

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 23:58:52 ; Search time 2913 Seconds
(without alignments)
12837.411 Million cell updates/sec

Title: US-09-659-860a-3
Perfect score: 2309
Sequence: 1 gagagacgtgcacgtccca.....gattaaaaatgtgtgtctt 2309

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 102860

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 1000 summaries

EST:*

1: em_estda:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vit:*
22: em_gss_fun:*
23: em_gss_man:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	22.6	1.0	45	17	AZ772088 1M0574P09
C 2	22	1.0	46	17	AZ857401 2M0162M07
C 3	22	1.0	47	17	AZ592788 1M0403P22
C 4	22	1.0	50	17	AZ458729 1M0263N06
C 5	21.8	0.9	50	9	AU103152 AU103152
C 6	21.6	0.9	40	17	AZ474054 1M0290K14

C 7	21.6	0.9	47	9	AU254247 AU254247
C 8	21.4	0.9	49	9	A1350847 qtl1e08.x
C 9	21	0.9	50	14	T25053 EST628.Huma
C 10	20.8	0.9	49	12	BG179823 602329028
C 11	20.8	0.9	49	14	W52971 zc97d11.r1
C 12	20.6	0.9	33	17	AZ788166 2M0035P03
C 13	20.6	0.9	41	14	H59040 yr40f09.s1
C 14	20.6	0.9	43	17	AZ314208 1M0030H21
C 15	20.6	0.9	49	9	A1973603 sd07b05.y
C 16	20.4	0.9	36	9	AU259306 AU259306
C 17	20.4	0.9	46	17	TA130G070
C 18	20.4	0.9	48	12	BG667239
C 19	20.4	0.9	49	9	AA505166
C 20	20.4	0.9	50	9	AU104178
C 21	20.4	0.9	50	17	AZ617534
C 22	20.2	0.9	42	14	C01292 HUMG5000456
C 23	20.2	0.9	46	9	AA946759
C 24	20.2	0.9	46	17	AZ498067 1M0335J12
C 25	20	0.9	38	17	AZ601365
C 26	20	0.9	41	17	AZ772635
C 27	20	0.9	46	17	AL757412 Arabidops
C 28	20	0.9	47	17	AZ823735 2M0097N19
C 29	20	0.9	48	17	BH852315 SALK_0744
C 30	20	0.9	49	17	AL755942 Arabidops
C 31	19.8	0.9	36	9	AU255361
C 32	19.8	0.9	39	17	AZ424159 1M0203D07
C 33	19.8	0.9	45	9	AU267061 AU267061
C 34	19.8	0.9	45	12	BF732129 EST-NGR-1
C 35	19.8	0.9	45	17	AZ791851 2M0041K20
C 36	19.8	0.9	47	17	BH855527 SALK_0770
C 37	19.8	0.9	49	9	AU394062 AU394062
C 38	19.8	0.9	50	9	AU106951 AU106951
C 39	19.8	0.9	50	13	B1910989 603069394
C 40	19.6	0.8	37	9	AU265147 AU265147
C 41	19.6	0.8	40	9	AA137304 mg80b07.r
C 42	19.6	0.8	43	13	B1834296 603084315
C 43	19.6	0.8	48	13	B033490 B033490
C 44	19.6	0.8	48	13	B083933 B083933
C 45	19.6	0.8	49	9	AA835093 ak63b06.s
C 46	19.6	0.8	50	9	AU103566 AU103566
C 47	19.6	0.8	50	9	AU103568 AU103568
C 48	19.6	0.8	50	13	B1175092 OSTR007H7
C 49	19.6	0.8	50	17	AZ950287 2M021K17
C 50	19.6	0.8	50	17	BH221751 100610380
C 51	19.4	0.8	37	17	BH792357 SALK_0640
C 52	19.4	0.8	41	17	AI167547 ox67h12.s
C 53	19.4	0.8	42	9	AA581390 nd88e09.s
C 54	19.4	0.8	43	9	AA283040 ztl6d06.s
C 55	19.4	0.8	44	17	AC021165
C 56	19.4	0.8	46	9	A1653818
C 57	19.4	0.8	46	14	T25667 EST00536.Eq
C 58	19.4	0.8	49	14	R95088 Y445h04.s1
C 59	19.4	0.8	49	17	AZ769070 1M0569D24
C 60	19.4	0.8	50	9	AA607953 vm39h06.r
C 61	19.4	0.8	50	17	TA230E010
C 62	19.2	0.8	40	17	AL764003 Arabidops
C 63	19.2	0.8	41	13	B1452713 603169931
C 64	19.2	0.8	41	17	AZ951455 2M0215H22
C 65	19.2	0.8	41	17	BH863255 SALK_0935
C 66	19.2	0.8	44	17	BH806014 1008063G1
C 67	19.2	0.8	45	17	AZ602556 1M0421E20
C 68	19.2	0.8	46	9	A1085448
C 69	19.2	0.8	46	17	BH806081 1008064D1
C 70	19.2	0.8	48	9	AU254949 AU254949
C 71	19.2	0.8	49	12	BE916026 601665326
C 72	19.2	0.8	50	9	A1624136 ts26c11.x
C 73	19.2	0.8	50	10	AY967273 AY967273
C 74	19.2	0.8	51	17	AZ486263 1M0314H11
C 75	19	0.8	39	17	BH864196 SALK_0955
C 76	19	0.8	43	9	AA936855 o151b06.s
C 77	19	0.8	44	12	BG688757 602787589
C 78	19	0.8	45	17	AZ504116 1M0344K08
C 79	19	0.8	46	9	AA828238 ob55a07.s

C 80	19	0.8	46	9	AA916623	AA916623 om05g05.s	153	18.6	0.8	49	9	AA798166	AA798166 vx67g05.r
C 81	19	0.8	46	9	AU269071	AU269071	154	18.6	0.8	49	9	AA855774	AA855774 vw74g02.i
C 82	19	0.8	46	17	TA369E01P	TA369E01P	C 155	18.6	0.8	49	10	AV742042	AV742042 av742042
C 83	19	0.8	47	17	BH86384	BH86384 SALK_1012	C 156	18.6	0.8	49	17	AZ576556	AZ576556 AST-T11C0
C 84	19	0.8	49	9	AU268128	AU268128	C 157	18.6	0.8	49	17	BH791118	BH791118 SALK_0587
C 85	19	0.8	49	14	H92807	H92807 yf90a12..r1	C 158	18.6	0.8	50	9	AU103157	AU103157
C 86	19	0.8	50	9	AU107724	AU107724	C 159	18.6	0.8	50	9	AU106264	AU106264
C 87	19	0.8	50	17	AZ645588	AZ645588 IM0511D09	C 160	18.6	0.8	50	9	AU107722	AU107722
C 88	19	0.8	50	17	AZ799040	AZ799040 2M0056L09	C 161	18.6	0.8	50	17	AZ621023	AZ621023 IM0454C04
C 89	19	0.8	50	17	BH855442	BH855442 SALK_0985	C 162	18.6	0.8	50	17	BH865870	BH865870 SALK_1000
C 90	18.8	0.8	35	9	AU268980	AU268980	C 163	18.4	0.8	32	17	AZ793379	AZ793379 2M0046P01
C 91	18.8	0.8	40	17	AZ486679	AZ486679 IM0314B23	C 164	18.4	0.8	36	17	AZ800600	AZ800600
C 92	18.8	0.8	43	17	BH626765	BH626765 1007112H0	C 165	18.4	0.8	35	17	AA878205	AA878205 oee6a01.s
C 93	18.8	0.8	43	17	BH632224	BH632224 1007094C0	C 166	18.4	0.8	44	17	AZ428520	AZ428520 IM0205H10
C 94	18.8	0.8	43	17	BH632235	BH632235 1007094C0	C 167	18.4	0.8	45	17	AA722052	AA722052 zh18f01.s
C 95	18.8	0.8	44	17	AZ433032	AZ433032 IM0218M12	C 168	18.4	0.8	45	17	AZ810468	AZ810468 2M0076E02
C 96	18.8	0.8	45	17	BH632327	BH632327 1007094E1	C 169	18.4	0.8	46	14	N44233	N44233 yy31c08..r1
C 97	18.8	0.8	45	17	BH801867	BH801867 1008115E0	C 170	18.4	0.8	46	17	AZ339864	AZ339864 IM0071G05
C 98	18.8	0.8	46	9	A1124130	A1124130 SMOVL3CAN	C 171	18.4	0.8	46	17	AL753248	AL753248
C 99	18.8	0.8	46	17	BH798631	BH798631 1008121E1	C 172	18.4	0.8	49	9	A1205223	A1205223 a08b01.x
C 100	18.8	0.8	46	17	BH801816	BH801816 1008115A0	C 173	18.4	0.8	49	14	R86483	R86483 RABEST057T
C 101	18.8	0.8	47	17	BH626648	BH626648 1007111G0	C 174	18.4	0.8	50	14	BQ090608	BQ090608 ku17g02.y
C 102	18.8	0.8	47	17	BH632190	BH632190 1007094A0	C 175	18.4	0.8	50	14	R89327	R89327 yg01d05..s1
C 103	18.8	0.8	47	17	AL771893	AL771893	C 176	18.4	0.8	50	14	T11436	T11436 CHR90002.ch
C 104	18.8	0.8	48	12	BE159807	BE159807	C 177	18.4	0.8	50	14	T11458	T11458 CHR90024.ch
C 105	18.8	0.8	49	9	AL649742	AL649742	C 178	18.4	0.8	50	14	BH856879	BH856879 SALK_0790
C 106	18.8	0.8	49	17	AZ767999	AZ767999 IM0567B16	C 179	18.4	0.8	37	9	A143659	A143659 lh35a09.x
C 107	18.8	0.8	49	17	BH624457	BH624457 1007078E1	C 180	18.2	0.8	39	14	H55136	H55136 CHR220075.C
C 108	18.8	0.8	49	17	BH855006	BH855006 SALK_0972	C 181	18.2	0.8	40	13	B1834374	B1834374 603084415
C 109	18.8	0.8	50	9	AJ500405	AJ500405	C 182	18.2	0.8	41	9	AU011117	AU011117
C 110	18.8	0.8	50	9	AU102879	AU102879	C 183	18.2	0.8	41	10	AM248967	AM248967 2819506.3
C 111	18.8	0.8	50	10	AM632974	AM632974 b102d06.x	C 184	18.2	0.8	44	9	AZ303870	AZ303870 IM0003J12
C 112	18.8	0.8	50	13	BF029726	BF029726 601556B15	C 185	18.2	0.8	44	17	AZ321551	AZ321551 IM0042T12
C 113	18.8	0.8	50	13	BJ066224	BJ066224	C 186	18.2	0.8	44	17	AM251061	AM251061 2822175.3
C 114	18.8	0.8	50	17	BH631106	BH631106 1007096H0	C 187	18.2	0.8	46	10	AM251061	AM251061 2822175.3
C 115	18.8	0.8	50	17	BH636800	BH636800	C 188	18.2	0.8	46	13	BJ055134	BJ055134 BJ055134
C 116	18.8	0.8	50	17	BH636973	BH636973 1008013C0	C 189	18.2	0.8	46	14	U44363	U44363 ENU44363.A5
C 117	18.8	0.8	50	17	BH796223	BH796223 1008085F0	C 190	18.2	0.8	46	17	AZ588863	AZ588863 IM0397P23
C 118	18.8	0.8	50	17	BH796265	BH796265 1008085F0	C 191	18.2	0.8	47	14	D20660	D20660 HUMS01636
C 119	18.8	0.8	50	17	BH797051	BH797051 1008086F0	C 192	18.2	0.8	47	17	AZ786064	AZ786064 2M0030G22
C 120	18.8	0.8	50	17	BH797292	BH797292 1008087F0	C 193	18.2	0.8	48	9	A1125418	A1125418 qd93c04.x
C 121	18.8	0.8	50	17	BH797605	BH797605 1008088G1	C 194	18.2	0.8	48	9	AL587964	AL587964
C 122	18.8	0.8	50	17	BH797769	BH797769 1008095B0	C 195	18.2	0.8	48	10	AV834599	AV834599 AV834599
C 123	18.8	0.8	50	17	BH797946	BH797946 1008096F0	C 196	18.2	0.8	48	17	AZ820860	AZ820860 2M0093B22
C 124	18.8	0.8	50	17	BH799504	BH799504 1008109A0	C 197	18.2	0.8	49	9	AA860637	AA860637 a182d10.s
C 125	18.8	0.8	50	17	BH799566	BH799566 1008109C0	C 198	18.2	0.8	49	9	AU270766	AU270766 AU270766
C 126	18.8	0.8	50	17	BH800507	BH800507 1008125B0	C 199	18.2	0.8	49	17	AZ514068	AZ514068 IM0360C09
C 127	18.8	0.8	50	17	BH801937	BH801937 1008122B0	C 200	18.2	0.8	49	17	AZ771132	AZ771132 IM0573002
C 128	18.8	0.8	50	17	BH802654	BH802654 1008101D0	C 201	18.2	0.8	49	17	BH847226	BH847226 SALK_0446
C 129	18.8	0.8	50	17	BH802749	BH802749 1008101H0	C 202	18.2	0.8	50	9	AU103478	AU103478
C 130	18.8	0.8	50	17	BH804538	BH804538 1008102H0	C 203	18.2	0.8	50	9	AU103770	AU103770
C 131	18.8	0.8	50	17	BH804583	BH804583 1008080C0	C 204	18.2	0.8	50	9	AU103775	AU103775
C 132	18.8	0.8	50	17	BH805635	BH805635 1008061F0	C 205	18.2	0.8	50	9	AU103983	AU103983
C 133	18.8	0.8	50	17	BH805931	BH805931 1008063B0	C 206	18.2	0.8	50	9	AU104426	AU104426
C 134	18.8	0.8	50	17	BH805953	BH805953 1008063C0	C 207	18.2	0.8	50	9	AU104428	AU104428
C 135	18.8	0.8	50	17	BH805964	BH805964 1008063D0	C 208	18.2	0.8	50	9	AU107371	AU107371
C 136	18.8	0.8	50	17	BH806092	BH806092 1008064E0	C 209	18.2	0.8	34	13	BH810113	BH810113 SALK_0409
C 137	18.8	0.8	50	17	BH806108	BH806108 1008064F0	C 210	18	0.8	35	9	AL634492	AL634492
C 138	18.8	0.8	50	17	BH806125	BH806125 1008064G0	C 211	18	0.8	35	17	AZ783571	AZ783571 2M0025024
C 139	18.8	0.8	50	17	BH807299	BH807299 1008064G0	C 212	18	0.8	35	17	AZ825655	AZ825655 2M00500P23
C 140	18.8	0.8	50	17	BH807530	BH807530 1008069E0	C 213	18	0.8	37	14	AA912402	AA912402 o199g09.s
C 141	18.6	0.8	36	14	T81822	T81822 yd93g06..s1	C 214	18	0.8	37	14	N48280	N48280 yz05h01..s1
C 142	18.6	0.8	36	17	TA270H08P	TA270H08P	C 215	18	0.8	39	17	AZ576137	AZ576137 AST-T33E0
C 143	18.6	0.8	42	12	BG896895	BG896895 HOA58-1-H	C 216	18	0.8	40	17	AL771426	AL771426
C 144	18.6	0.8	42	12	BF139151	BF139151 601784191	C 217	18	0.8	41	17	AZ480317	AZ480317
C 145	18.6	0.8	42	17	AZ775850	AZ775850 2M0009M05	C 218	18	0.8	42	17	AZ514372	AZ514372
C 146	18.6	0.8	44	9	AL594306	AL594306	C 219	18	0.8	43	9	A1227107	A1227107 u112a01.y
C 147	18.6	0.8	45	2	HSM002460	HSM002460	C 220	18	0.8	43	9	A1540308	A1540308 t934e02.x
C 148	18.6	0.8	46	10	AV847044	AV847044	C 221	18	0.8	44	17	AL768905	AL768905
C 149	18.6	0.8	46	13	BJ080962	BJ080962	C 222	18	0.8	44	9	AU009914	AU009914
C 150	18.6	0.8	47	9	AU264538	AU264538	C 223	18	0.8	44	17	AZ387197	AZ387197 IM0146020
C 151	18.6	0.8	47	13	BJ039490	BJ039490	C 224	18	0.8	46	9	AL588816	AL588816
C 152	18.6	0.8	49	9	AA777336	AA777336 z192h07.s	C 225	18	0.8	46	9	AL588816	AL588816

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C 226	18	0.8	46	17	A2846167	A2846167 2M0146D15	C 299	17.8	0.8	50	9	AU104979	AU104979 AU104979
C 227	18	0.8	46	17	HSWC43F06	X88058 H.sapiens D	C 300	17.8	0.8	50	9	AU104980	AU104980 AU104980
C 228	18	0.8	46	17	TA5D04P	AL452288 T. brucei	C 301	17.8	0.8	50	9	AU104981	AU104981 AU104981
C 229	18	0.8	47	9	AU268330	AU268330 AU270701	C 302	17.8	0.8	50	9	AU104985	AU104985 AU104985
C 230	18	0.8	47	9	AU270701	D18780 M05GS00496	C 303	17.8	0.8	50	9	AU105880	AU105880 AU105880
C 231	18	0.8	47	14	TA32A07P	AL458717 T. brucei	C 304	17.8	0.8	50	9	AU106015	AU106015 AU106015
C 232	18	0.8	48	13	BM014534	BM014534 603640331	C 305	17.8	0.8	50	9	AU106058	AU106058 AU106058
C 233	18	0.8	48	13	BM014534	W10946 ma46b10..r1	C 306	17.8	0.8	50	9	AU107179	AU107179 AU107179
C 234	18	0.8	49	14	W10946	AL279722 G153901.x	C 307	17.8	0.8	50	9	AU107718	AU107718 AU107718
C 235	18	0.8	49	9	AL279722	BC723554 602694227	C 308	17.8	0.8	50	9	AU107720	AU107720 AU107720
C 236	18	0.8	49	12	BC723554	BO704655 Bn01_03h1	C 309	17.8	0.8	50	9	AU107721	AU107721 AU107721
C 237	18	0.8	49	14	BO704655	A2852964 2M0155B01	C 310	17.8	0.8	50	9	AA574989	AA574989 AA574989
C 238	18	0.8	49	17	A2852964	AA120437 ma47a11..T	C 311	17.8	0.8	50	10	AA574989	AA574989 AA574989
C 239	18	0.8	50	9	AA120437	AU103561 AU103561	C 312	17.8	0.8	50	13	AA574989	AA574989 AA574989
C 240	18	0.8	50	9	AU103561	AU103562 AU103562	C 313	17.8	0.8	50	14	AA574989	AA574989 AA574989
C 241	18	0.8	50	9	AU103562	BE306432 601103378	C 314	17.8	0.8	50	17	AA574989	AA574989 AA574989
C 242	18	0.8	50	10	BE306432	BE306432 602694646	C 315	17.8	0.8	50	17	AA574989	AA574989 AA574989
C 243	18	0.8	50	12	BE306432	BE306432 602694646	C 316	17.8	0.8	50	17	AA574989	AA574989 AA574989
C 244	18	0.8	50	17	A2486573	A2486573 1M0332P09	C 317	17.8	0.8	50	17	AA574989	AA574989 AA574989
C 245	18	0.8	50	17	A2486573	D19564 M05GS00968	C 318	17.8	0.8	50	17	AA574989	AA574989 AA574989
C 246	18	0.8	37	14	D19564	A2471063 1M0285005	C 319	17.8	0.8	50	17	AA574989	AA574989 AA574989
C 247	17.8	0.8	38	17	A2471063	AU266702 AU266702	C 320	17.6	0.8	38	17	AA574989	AA574989 AA574989
C 248	17.8	0.8	39	9	AU266702	AU266702 AU266702	C 321	17.6	0.8	40	9	AA574989	AA574989 AA574989
C 249	17.8	0.8	39	9	AU266702	AU266702 AU266702	C 322	17.6	0.8	40	9	AA574989	AA574989 AA574989
C 250	17.8	0.8	39	17	AU266702	AU266702 AU266702	C 323	17.6	0.8	40	9	AA574989	AA574989 AA574989
C 251	17.8	0.8	40	9	AA953211	AA953211 CO07C08..s	C 324	17.6	0.8	41	9	AA574989	AA574989 AA574989
C 252	17.8	0.8	40	9	AA953211	AU012364 AU012364	C 325	17.6	0.8	41	17	AA574989	AA574989 AA574989
C 253	17.8	0.8	41	17	BM003398	BM003398 1008100A0	C 326	17.6	0.8	42	13	AA574989	AA574989 AA574989
C 254	17.8	0.8	43	9	AA103421	AA103421 SMOVL3CAN	C 327	17.6	0.8	42	13	AA574989	AA574989 AA574989
C 255	17.8	0.8	43	9	AA103421	AA103421 SMOVL3CAN	C 328	17.6	0.8	42	13	AA574989	AA574989 AA574989
C 256	17.8	0.8	43	10	AA9846880	AA9846880 AV846880	C 329	17.6	0.8	43	10	AA574989	AA574989 AA574989
C 257	17.8	0.8	43	10	AA9846880	AA9846880 AV846880	C 330	17.6	0.8	43	14	AA574989	AA574989 AA574989
C 258	17.8	0.8	43	14	AA9846880	AA9846880 AV846880	C 331	17.6	0.8	43	14	AA574989	AA574989 AA574989
C 259	17.8	0.8	43	17	AA9846880	AA9846880 AV846880	C 332	17.6	0.8	43	17	AA574989	AA574989 AA574989
C 260	17.8	0.8	43	17	AA9846880	AA9846880 AV846880	C 333	17.6	0.8	43	17	AA574989	AA574989 AA574989
C 261	17.8	0.8	43	17	AA9846880	AA9846880 AV846880	C 334	17.6	0.8	43	17	AA574989	AA574989 AA574989
C 262	17.8	0.8	43	17	AA9846880	AA9846880 AV846880	C 335	17.6	0.8	44	9	AA574989	AA574989 AA574989
C 263	17.8	0.8	43	12	AA9846880	AA9846880 AV846880	C 336	17.6	0.8	44	17	AA574989	AA574989 AA574989
C 264	17.8	0.8	45	9	AA9846880	AA9846880 AV846880	C 337	17.6	0.8	45	17	AA574989	AA574989 AA574989
C 265	17.8	0.8	45	10	AA9846880	AA9846880 AV846880	C 338	17.6	0.8	45	17	AA574989	AA574989 AA574989
C 266	17.8	0.8	45	10	AA9846880	AA9846880 AV846880	C 339	17.6	0.8	46	10	AA574989	AA574989 AA574989
C 267	17.8	0.8	45	17	AA9846880	AA9846880 AV846880	C 340	17.6	0.8	46	10	AA574989	AA574989 AA574989
C 268	17.8	0.8	45	17	AA9846880	AA9846880 AV846880	C 341	17.6	0.8	46	10	AA574989	AA574989 AA574989
C 269	17.8	0.8	46	17	AA9846880	AA9846880 AV846880	C 342	17.6	0.8	48	13	AA574989	AA574989 AA574989
C 270	17.8	0.8	46	17	AA9846880	AA9846880 AV846880	C 343	17.6	0.8	48	13	AA574989	AA574989 AA574989
C 271	17.8	0.8	46	17	AA9846880	AA9846880 AV846880	C 344	17.6	0.8	48	17	AA574989	AA574989 AA574989
C 272	17.8	0.8	47	9	AA9846880	AA9846880 AV846880	C 345	17.6	0.8	48	17	AA574989	AA574989 AA574989
C 273	17.8	0.8	47	10	AA9846880	AA9846880 AV846880	C 346	17.6	0.8	48	17	AA574989	AA574989 AA574989
C 274	17.8	0.8	47	17	AA9846880	AA9846880 AV846880	C 347	17.6	0.8	48	17	AA574989	AA574989 AA574989
C 275	17.8	0.8	47	17	AA9846880	AA9846880 AV846880	C 348	17.6	0.8	48	17	AA574989	AA574989 AA574989
C 276	17.8	0.8	48	14	AA9846880	AA9846880 AV846880	C 349	17.6	0.8	49	9	AA574989	AA574989 AA574989
C 277	17.8	0.8	48	14	AA9846880	AA9846880 AV846880	C 350	17.6	0.8	49	9	AA574989	AA574989 AA574989
C 278	17.8	0.8	48	17	AA9846880	AA9846880 AV846880	C 351	17.6	0.8	49	9	AA574989	AA574989 AA574989
C 279	17.8	0.8	48	17	AA9846880	AA9846880 AV846880	C 352	17.6	0.8	49	9	AA574989	AA574989 AA574989
C 280	17.8	0.8	48	17	AA9846880	AA9846880 AV846880	C 353	17.6	0.8	49	9	AA574989	AA574989 AA574989
C 281	17.8	0.8	48	17	AA9846880	AA9846880 AV846880	C 354	17.6	0.8	49	9	AA574989	AA574989 AA574989
C 282	17.8	0.8	48	17	AA9846880	AA9846880 AV846880	C 355	17.6	0.8	49	9	AA574989	AA574989 AA574989
C 283	17.8	0.8	48	17	AA9846880	AA9846880 AV846880	C 356	17.6	0.8	49	9	AA574989	AA574989 AA574989
C 284	17.8	0.8	48	17	AA9846880	AA9846880 AV846880	C 357	17.6	0.8	49	9	AA574989	AA574989 AA574989
C 285	17.8	0.8	49	9	AA9846880	AA9846880 AV846880	C 358	17.6	0.8	49	9	AA574989	AA574989 AA574989
C 286	17.8	0.8	49	12	AA9846880	AA9846880 AV846880	C 359	17.6	0.8	49	9	AA574989	AA574989 AA574989
C 287	17.8	0.8	49	13	AA9846880	AA9846880 AV846880	C 360	17.6	0.8	50	9	AA574989	AA574989 AA574989
C 288	17.8	0.8	49	14	AA9846880	AA9846880 AV846880	C 361	17.6	0.8	50	9	AA574989	AA574989 AA574989
C 289	17.8	0.8	49	17	AA9846880	AA9846880 AV846880	C 362	17.6	0.8	50	9	AA574989	AA574989 AA574989
C 290	17.8	0.8	50	9	AA9846880	AA9846880 AV846880	C 363	17.6	0.8	50	9	AA574989	AA574989 AA574989
C 291	17.8	0.8	50	9	AA9846880	AA9846880 AV846880	C 364	17.6	0.8	50	9	AA574989	AA574989 AA574989
C 292	17.8	0.8	50	9	AA9846880	AA9846880 AV846880	C 365	17.6	0.8	50	10	AA574989	AA574989 AA574989
C 293	17.8	0.8	50	9	AA9846880	AA9846880 AV846880	C 366	17.6	0.8	50	10	AA574989	AA574989 AA574989
C 294	17.8	0.8	50	9	AA9846880	AA9846880 AV846880	C 367	17.6	0.8	50	10	AA574989	AA574989 AA574989
C 295	17.8	0.8	50	9	AA9846880	AA9846880 AV846880	C 368	17.6	0.8	50	10	AA574989	AA574989 AA574989
C 296	17.8	0.8	50	9	AA9846880	AA9846880 AV846880	C 369	17.6	0.8	50	13	AA574989	AA574989 AA574989
C 297	17.8	0.8	50	9	AA9846880	AA9846880 AV846880	C 370	17.6	0.8	50	13	AA574989	AA574989 AA574989
C 298	17.8	0.8	50	9	AA9846880	AA9846880 AV846880	C 371	17.6	0.8	50	14	AA574989	AA574989 AA574989

372	17.4	0.8	28	17	A2387822	IM0147D23	C 445	17.2	0.7	41	13	B1550138
373	17.4	0.8	31	10	AM248330	2820380.5	446	17.2	0.7	41	17	A2466566
374	17.4	0.8	33	17	TAR08C110	AL461346 T. brucei	447	17.2	0.7	41	17	BH809716
375	17.4	0.8	36	17	A2314238	IM0030N24	448	17.2	0.7	41	17	BH846279
376	17.4	0.8	37	9	AA056537	AA056537 zK80a05.s	449	17.2	0.7	41	17	BH846279
377	17.4	0.8	37	9	AA056537	AA056537 zK80a05.s	450	17.2	0.7	41	17	TA77DD30Q
378	17.4	0.8	38	17	A2453551	AA056537 zK80a05.s	451	17.2	0.7	42	14	TS7173
379	17.4	0.8	38	17	A2453551	AA056537 zK80a05.s	452	17.2	0.7	42	14	TS7173
380	17.4	0.8	39	17	BH861103	BH861103 SALK_0341	453	17.2	0.7	42	17	BH804013
381	17.4	0.8	40	17	A2615013	BH861103 SALK_0341	454	17.2	0.7	43	9	AT097835
382	17.4	0.8	40	17	A2615013	BH861103 SALK_0341	455	17.2	0.7	43	13	B1916603
383	17.4	0.8	40	17	A2615013	BH861103 SALK_0341	456	17.2	0.7	43	17	AT097835
384	17.4	0.8	40	17	A2615013	BH861103 SALK_0341	457	17.2	0.7	44	9	A2477149
385	17.4	0.8	43	9	AT000712	AT000712 oxv0703.s	458	17.2	0.7	44	14	N78262
386	17.4	0.8	43	9	AT000712	AT000712 oxv0703.s	459	17.2	0.7	44	14	N78262
387	17.4	0.8	43	17	CNS07EPW	AT000712 oxv0703.s	460	17.2	0.7	44	17	A2657241
388	17.4	0.8	43	17	TA243F12P	AT000712 oxv0703.s	461	17.2	0.7	45	14	A2657241
389	17.4	0.8	44	9	AT0268768	AT000712 oxv0703.s	462	17.2	0.7	45	14	AT0268768
390	17.4	0.8	44	9	AT0268768	AT000712 oxv0703.s	463	17.2	0.7	45	14	AT0268768
391	17.4	0.8	44	13	BJ050937	AT000712 oxv0703.s	464	17.2	0.7	45	17	AT0268768
392	17.4	0.8	45	13	BJ050937	AT000712 oxv0703.s	465	17.2	0.7	45	17	AT0268768
393	17.4	0.8	45	13	BJ050937	AT000712 oxv0703.s	466	17.2	0.7	46	9	AA128521
394	17.4	0.8	46	17	A2659768	AT000712 oxv0703.s	467	17.2	0.7	46	10	AA128521
395	17.4	0.8	46	17	A2659768	AT000712 oxv0703.s	468	17.2	0.7	46	10	AA128521
396	17.4	0.8	46	17	A2659768	AT000712 oxv0703.s	469	17.2	0.7	46	10	AA128521
397	17.4	0.8	47	10	AA956026	AT000712 oxv0703.s	470	17.2	0.7	46	14	AA956026
398	17.4	0.8	47	10	AA956026	AT000712 oxv0703.s	471	17.2	0.7	46	14	AA956026
399	17.4	0.8	47	17	BH637261	AT000712 oxv0703.s	472	17.2	0.7	46	17	AA956026
400	17.4	0.8	47	17	BH637261	AT000712 oxv0703.s	473	17.2	0.7	46	17	AA956026
401	17.4	0.8	47	17	BH790372	AT000712 oxv0703.s	474	17.2	0.7	46	17	AA956026
402	17.4	0.8	47	17	BH790372	AT000712 oxv0703.s	475	17.2	0.7	46	17	AA956026
403	17.4	0.8	47	17	BH802737	AT000712 oxv0703.s	476	17.2	0.7	47	13	BH802737
404	17.4	0.8	47	17	BH802737	AT000712 oxv0703.s	477	17.2	0.7	47	13	BH802737

C 518	17	0.7	40	9	AA412136	AA412136	zt94a11.r	C 591	17	0.7	50	9	AU2671121	AU2671121	AU2671121
C 519	17	0.7	41	12	BE889658	BE889658	601512681	C 592	17	0.7	50	9	AU268417	AU268417	AU268417
C 520	17	0.7	41	17	AZ430737	AZ430737	1M0215A24	C 593	17	0.7	50	10	AV960925	AV960925	AV960925
C 521	17	0.7	41	17	AZ793496	AZ793496	2M0046116	C 594	17	0.7	50	13	BI436978	BI436978	BI436978
C 522	17	0.7	41	17	AL765652	AL765652	Arabidops	C 595	17	0.7	50	13	BI917015	BI917015	BI917015
C 523	17	0.7	41	17	AL766161	AL766161	Arabidops	C 596	17	0.7	50	14	BQ393428	BQ393428	BQ393428
C 524	17	0.7	42	13	BQ39854	BQ39854	Arabidops	C 597	17	0.7	50	17	AZ434153	AZ434153	AZ434153
C 525	17	0.7	42	14	C00698	C00698	HUMS000825	C 598	17	0.7	50	17	AZ476239	AZ476239	AZ476239
C 526	17	0.7	42	17	AZ645652	AZ645652	1M0511P07	C 599	17	0.7	50	17	AZ602063	AZ602063	AZ602063
C 527	17	0.7	42	17	TA67E02P	TA67E02P	AL4618018 T. brucei	C 600	17	0.7	50	17	AZ665355	AZ665355	AZ665355
C 528	17	0.7	43	17	TA84G09Q	TA84G09Q	AL461180 T. brucei	C 601	17	0.7	50	17	AZ776790	AZ776790	AZ776790
C 529	17	0.7	44	9	AU268392	AU268392	AU268392 AU268392	C 602	17	0.7	50	17	BH865986	BH865986	BH865986
C 530	17	0.7	44	9	AU268634	AU268634	AU268634 AU268634	C 603	17	0.7	50	17	BH865986	BH865986	BH865986
C 531	17	0.7	45	9	AA042885	AA042885	AA042885 2K56905.S	C 604	16.8	0.7	32	17	AZ458690	AZ458690	AZ458690
C 532	17	0.7	45	9	AU255677	AU255677	AU255677 AU255677	C 605	16.8	0.7	32	17	AL756371	AL756371	AL756371
C 533	17	0.7	45	9	AU258887	AU258887	AU258887 AU258887	C 606	16.8	0.7	33	17	AZ366238	AZ366238	AZ366238
C 534	17	0.7	45	12	BF691166	BF691166	BF691166 602247257	C 607	16.8	0.7	34	17	AZ433971	AZ433971	AZ433971
C 535	17	0.7	45	14	C01391	C01391	C01391 HUMS000837	C 608	16.8	0.7	34	17	AL769411	AL769411	AL769411
C 536	17	0.7	45	14	T01020	T01020	T01020 ycl17c07.r1	C 609	16.8	0.7	37	9	AU254241	AU254241	AU254241
C 537	17	0.7	45	17	AZ773812	AZ773812	AZ773812 2M0001M03	C 610	16.8	0.7	37	9	AU254241	AU254241	AU254241
C 538	17	0.7	46	9	AA873719	AA873719	AA873719 ocl51H08.S	C 611	16.8	0.7	39	13	BQ049570	BQ049570	BQ049570
C 539	17	0.7	46	9	AI958214	AI958214	AI958214 fc92f08.Y	C 612	16.8	0.7	39	17	BH235137	BH235137	BH235137
C 540	17	0.7	46	9	AA152923	AA152923	AA152923 mc89N01.r	C 613	16.8	0.7	39	17	BH790425	BH790425	BH790425
C 541	17	0.7	46	17	AZ487823	AZ487823	AZ487823 1M0317B17	C 614	16.8	0.7	39	17	BH811645	BH811645	BH811645
C 542	17	0.7	46	17	BH811331	BH811331	BH811331 SALK_0584	C 615	16.8	0.7	39	17	BH846328	BH846328	BH846328
C 543	17	0.7	47	9	AL627881	AL627881	AL627881 AL627881	C 616	16.8	0.7	39	17	BH846594	BH846594	BH846594
C 544	17	0.7	47	9	AU267623	AU267623	AU267623 AU267623	C 617	16.8	0.7	40	9	AI056002	AI056002	AI056002
C 545	17	0.7	47	9	AU270701	AU270701	AU270701 AU270701	C 618	16.8	0.7	40	10	AV834221	AV834221	AV834221
C 546	17	0.7	47	10	AM248741	AM248741	AM248741 2820783.3	C 619	16.8	0.7	40	17	AZ308989	AZ308989	AZ308989
C 547	17	0.7	47	13	BQ045556	BQ045556	BQ045556 BQ045556	C 620	16.8	0.7	40	17	BH853060	BH853060	BH853060
C 548	17	0.7	47	17	AZ474384	AZ474384	AZ474384 1M0290C024	C 621	16.8	0.7	41	17	AZ805636	AZ805636	AZ805636
C 549	17	0.7	47	17	AZ946128	AZ946128	AZ946128 2M0207115	C 622	16.8	0.7	41	17	AZ805636	AZ805636	AZ805636
C 550	17	0.7	47	17	BH809693	BH809693	BH809693 SALK_0049	C 623	16.8	0.7	41	17	BH802322	BH802322	BH802322
C 551	17	0.7	47	17	BH862048	BH862048	BH862048 SALK_0886	C 624	16.8	0.7	42	17	AZ576704	AZ576704	AZ576704
C 552	17	0.7	48	9	AU266602	AU266602	AU266602 AU266602	C 625	16.8	0.7	42	17	BH855285	BH855285	BH855285
C 553	17	0.7	48	14	C21451	C21451	C21451 HUMS001043	C 626	16.8	0.7	43	9	AA968566	AA968566	AA968566
C 554	17	0.7	48	14	D18689	D18689	D18689 HUMS001751	C 627	16.8	0.7	43	9	AI089212	AI089212	AI089212
C 555	17	0.7	48	17	AZ480319	AZ480319	AZ480319 1M0301C16	C 628	16.8	0.7	43	9	AI591265	AI591265	AI591265
C 556	17	0.7	48	17	AZ792044	AZ792044	AZ792044 2M0043B17	C 629	16.8	0.7	43	9	AZ475536	AZ475536	AZ475536
C 557	17	0.7	48	17	BH789486	BH789486	BH789486 SALK_0297	C 630	16.8	0.7	44	17	AZ475536	AZ475536	AZ475536
C 558	17	0.7	48	17	BH814028	BH814028	BH814028 SALK_0656	C 631	16.8	0.7	44	9	AI570343	AI570343	AI570343
C 559	17	0.7	48	17	HSC06F06	HSC06F06	HSC06F06 HSC06F06	C 632	16.8	0.7	44	9	AU257585	AU257585	AU257585
C 560	17	0.7	49	9	AI357699	AI357699	AI357699 qv17f04.x	C 633	16.8	0.7	44	10	AV842450	AV842450	AV842450
C 561	17	0.7	49	9	AA116935	AA116935	AA116935 mv22g01.r	C 634	16.8	0.7	44	13	BI094759	BI094759	BI094759
C 562	17	0.7	49	9	AI664277	AI664277	AI664277 ue83g05.x	C 635	16.8	0.7	44	13	BI080612	BI080612	BI080612
C 563	17	0.7	49	9	AI931109	AI931109	AI931109 fc77a05.x	C 636	16.8	0.7	44	17	AZ439478	AZ439478	AZ439478
C 564	17	0.7	49	9	AI973920	AI973920	AI973920 sd13f09.Y	C 637	16.8	0.7	44	17	TA238B03Q	TA238B03Q	TA238B03Q
C 565	17	0.7	49	9	AA157965	AA157965	AA157965 z054h01.S	C 638	16.8	0.7	45	9	AA896459	AA896459	AA896459
C 566	17	0.7	49	9	AU254531	AU254531	AU254531 AU254531	C 639	16.8	0.7	45	9	AL779895	AL779895	AL779895
C 567	17	0.7	49	9	AA388129	AA388129	AA388129 vc86f05.r	C 640	16.8	0.7	45	9	AU256306	AU256306	AU256306
C 568	17	0.7	49	12	BF343486	BF343486	BF343486 602017592	C 641	16.8	0.7	45	14	D34826	D34826	D34826
C 569	17	0.7	49	13	BI839340	BI839340	BI839340 fs66c11.Y	C 642	16.8	0.7	45	17	AZ467950	AZ467950	AZ467950
C 570	17	0.7	49	14	W39280	W39280	W39280 zc76g04.r1	C 643	16.8	0.7	45	17	AZ955701	AZ955701	AZ955701
C 571	17	0.7	49	17	AZ789295	AZ789295	AZ789295 2M0036J19	C 644	16.8	0.7	46	9	AA915738	AA915738	AA915738
C 572	17	0.7	49	17	TA98D04Q	TA98D04Q	TA98D04Q T. brucei	C 645	16.8	0.7	46	9	AU256918	AU256918	AU256918
C 573	17	0.7	50	2	HS002946	HS002946	HS002946 HS002946	C 646	16.8	0.7	46	9	AA522160	AA522160	AA522160
C 574	17	0.7	50	9	AU102459	AU102459	AU102459 AU102459	C 647	16.8	0.7	46	13	BI0615738	BI0615738	BI0615738
C 575	17	0.7	50	9	AU102460	AU102460	AU102460 AU102460	C 648	16.8	0.7	46	14	AZ332059	AZ332059	AZ332059
C 576	17	0.7	50	9	AU102461	AU102461	AU102461 AU102461	C 649	16.8	0.7	46	17	AZ345887	AZ345887	AZ345887
C 577	17	0.7	50	9	AU102462	AU102462	AU102462 AU102462	C 650	16.8	0.7	46	17	AZ429913	AZ429913	AZ429913
C 578	17	0.7	50	9	AU102466	AU102466	AU102466 AU102466	C 651	16.8	0.7	46	17	AZ429913	AZ429913	AZ429913
C 579	17	0.7	50	9	AU102758	AU102758	AU102758 AU102758	C 652	16.8	0.7	46	17	AZ429913	AZ429913	AZ429913
C 580	17	0.7	50	9	AU102805	AU102805	AU102805 AU102805	C 653	16.8	0.7	46	17	AZ429913	AZ429913	AZ429913
C 581	17	0.7	50	9	AU102990	AU102990	AU102990 AU102990	C 654	16.8	0.7	46	17	AZ429913	AZ429913	AZ429913
C 582	17	0.7	50	9	AU103731	AU103731	AU103731 AU103731	C 655	16.8	0.7	46	17	AZ429913	AZ429913	AZ429913
C 583	17	0.7	50	9	AU103801	AU103801	AU103801 AU103801	C 656	16.8	0.7	46	17	AZ429913	AZ429913	AZ429913
C 584	17	0.7	50	9	AU103811	AU103811	AU103811 AU103811	C 657	16.8	0.7	46	17	BH885339	BH885339	BH885339
C 585	17	0.7	50	9	AU103817	AU103817	AU103817 AU103817	C 658	16.8	0.7	47	14	BH80650	BH80650	BH80650
C 586	17	0.7	50	9	AU104173	AU104173	AU104173 AU104173	C 659	16.8	0.7	47	17	AZ581244	AZ581244	AZ581244
C 587	17	0.7	50	9	AU104186	AU104186	AU104186 AU104186	C 660	16.8	0.7	47	17	AZ767279	AZ767279	AZ767279
C 588	17	0.7	50	9	AU106263	AU106263	AU106263 AU106263	C 661	16.8	0.7	47	17	AZ778260	AZ778260	AZ778260
C 589	17	0.7	50	9	AU107157	AU107157	AU107157 AU107157	C 662	16.8	0.7	47	17	AZ998783	AZ998783	AZ998783
C 590	17	0.7	50	9	AU107358	AU107358	AU107358 AU107358	C 663	16.8	0.7	47	17	BH848630	BH848630	BH848630

664	16.8	0.7	48	14	H47082	yp73905.s1	737	16.6	0.7	43	9	AA912350
665	16.8	0.7	48	17	BH792188	BH792188.SALK_0629	738	16.6	0.7	43	9	AA461694
666	16.8	0.7	48	17	BH811694	BH811694.SALK_0596	739	16.6	0.7	43	14	L46927
667	16.8	0.7	48	17	BH853315	BH853315.SALK_0744	740	16.6	0.7	43	17	AA2659678
668	16.8	0.7	48	17	AL764810	AL764810.Arabidops	741	16.6	0.7	43	17	AA2659678
669	16.8	0.7	48	17	HSC06F06	X88550.H.sapiens.D	742	16.6	0.7	43	17	TA18C110
670	16.8	0.7	49	9	AI052522	AI052522.v237f05.x	743	16.6	0.7	44	9	AA162616
671	16.8	0.7	49	9	AI920810	AI920810.w82d01.x	744	16.6	0.7	44	10	AA833320
672	16.8	0.7	49	12	BE970036	BE970036.wx38g07.x	745	16.6	0.7	44	17	AA663219
673	16.8	0.7	49	13	BM128139	BM128139.if10b06.y	746	16.6	0.7	44	17	AA663219
674	16.8	0.7	49	13	BM128139	BM128139.if10b06.y	747	16.6	0.7	44	17	AA663219
675	16.8	0.7	49	14	BM889473	BM889473.la02g05-	748	16.6	0.7	44	17	AA663219
676	16.8	0.7	49	14	H16724	H16724.ym22f11.s1	749	16.6	0.7	45	9	AA256306
677	16.8	0.7	49	17	AZ346760	AZ346760.IM0082P12	750	16.6	0.7	45	17	AA256306
678	16.8	0.7	49	17	AZ448959	AZ448959.IM0247A04	751	16.6	0.7	45	17	AA256306
679	16.8	0.7	49	17	AZ587341	AZ587341.IM0394O20	752	16.6	0.7	45	17	AA256306
680	16.8	0.7	50	9	AI337715	AI337715.pw6b10.x	753	16.6	0.7	45	17	TA120H12P
681	16.8	0.7	50	9	AU006647	AU006647.AU006647	754	16.6	0.7	46	9	AU259048
682	16.8	0.7	50	9	AU102228	AU102228.AU102228	755	16.6	0.7	46	10	AA841944
683	16.8	0.7	50	9	AU102526	AU102526.AU102526	756	16.6	0.7	46	14	H95347
684	16.8	0.7	50	9	AU102526	AU102526.AU102526	757	16.6	0.7	46	17	AZ440102
685	16.8	0.7	50	9	AU104583	AU104583.AU104583	758	16.6	0.7	46	17	AZ440102
686	16.8	0.7	50	9	AU105742	AU105742.AU105742	759	16.6	0.7	46	17	AZ440102
687	16.8	0.7	50	9	AU106157	AU106157.AU106157	760	16.6	0.7	46	17	BH810877
688	16.8	0.7	50	9	AU106217	AU106217.AU106217	761	16.6	0.7	46	17	BH810877
689	16.8	0.7	50	9	AU106981	AU106981.AU106981	762	16.6	0.7	46	17	BH812741
690	16.8	0.7	50	9	AU107428	AU107428.AU107428	763	16.6	0.7	46	17	BH812744
691	16.8	0.7	50	9	AU258139	AU258139.AU258139	764	16.6	0.7	46	17	TA23A070
692	16.8	0.7	50	10	AA847546	AA847546.AV847546	765	16.6	0.7	47	9	AA268330
693	16.8	0.7	50	10	AA847546	AA847546.AV847546	766	16.6	0.7	47	9	AA268330
694	16.8	0.7	50	13	BM142934	BM142934.rk76d10.y	767	16.6	0.7	47	10	AA059738
695	16.8	0.7	50	13	BM142934	BM142934.rk76d10.y	768	16.6	0.7	47	10	AA059738
696	16.8	0.7	50	13	BM142934	BM142934.rk76d10.y	769	16.6	0.7	47	13	AA250836
697	16.8	0.7	50	14	BQ26347	BQ26347.NTSC_ff09	770	16.6	0.7	47	17	AZ6607114
698	16.8	0.7	50	14	BQ26347	BQ26347.NTSC_ff09	771	16.6	0.7	47	17	AZ6607114
699	16.8	0.7	50	17	AZ347604	AZ347604.IM0083C13	772	16.6	0.7	47	17	AZ6607114
700	16.8	0.7	50	17	AZ621474	AZ621474.IM0454C08	773	16.6	0.7	47	17	AZ6607114
701	16.8	0.7	50	17	AZ830260	AZ830260.2M0109121	774	16.6	0.7	47	17	AZ6607114
702	16.8	0.7	50	17	BH846604	BH846604.SALK_0091	775	16.6	0.7	47	17	BH861810
703	16.8	0.7	50	17	BH846604	BH846604.SALK_0091	776	16.6	0.7	47	17	BH861810
704	16.8	0.7	50	17	DR18C10T	DR18C10T.Danio rer	777	16.6	0.7	47	17	AG019636
705	16.8	0.7	50	17	DR24E15S	DR24E15S.Danio rer	778	16.6	0.7	47	17	AL754141
706	16.8	0.7	50	17	DR24E15S	DR24E15S.Danio rer	779	16.6	0.7	47	17	AL754141
707	16.8	0.7	50	17	BI081179	BI081179.602879191	780	16.6	0.7	48	17	BE507210
708	16.8	0.7	50	17	AZ445446	AZ445446.AU255377	781	16.6	0.7	48	17	BE507210
709	16.8	0.7	50	17	AU255377	AU255377.AU255377	782	16.6	0.7	48	17	BE507210
710	16.8	0.7	50	17	BU076531	BU076531.BU076531	783	16.6	0.7	48	17	BE507210
711	16.8	0.7	50	17	BU076531	BU076531.BU076531	784	16.6	0.7	48	17	BE507210
712	16.8	0.7	50	17	CG1136	CG1136.HUMS000781	785	16.6	0.7	48	17	TA175A01P
713	16.8	0.7	50	17	BG529663	BG529663.602558102	786	16.6	0.7	48	17	TA175A01P
714	16.8	0.7	50	17	BH813453	BH813453.SALK_0642	787	16.6	0.7	49	9	AA915234
715	16.8	0.7	50	17	BH849452	BH849452.SALK_0697	788	16.6	0.7	49	9	AA915234
716	16.8	0.7	50	17	TA11C050	TA11C050.AZ431282	789	16.6	0.7	49	9	AA915234
717	16.8	0.7	50	17	AZ431282	AZ431282.IM0216D12	790	16.6	0.7	49	9	AA915234
718	16.8	0.7	50	17	AZ274766	AZ274766.2M0004G05	791	16.6	0.7	49	9	AA915234
719	16.8	0.7	50	17	AZ826607	AZ826607.2M0102P14	792	16.6	0.7	49	9	AA915234
720	16.8	0.7	50	17	AI005592	AI005592.ov15B02.s	793	16.6	0.7	49	9	AA915234
721	16.8	0.7	50	17	AI590572	AI590572.tw13h05.x	794	16.6	0.7	49	9	AA915234
722	16.8	0.7	50	17	AZ612625	AZ612625.IM0439C05	795	16.6	0.7	49	9	AA915234
723	16.8	0.7	50	17	BH862131	BH862131.SALK_0878	796	16.6	0.7	49	9	AA915234
724	16.8	0.7	50	17	BH865149	BH865149.SALK_0974	797	16.6	0.7	49	9	AA915234
725	16.8	0.7	50	17	H96953	H96953.yu01g06.t1	798	16.6	0.7	49	9	AA915234
726	16.8	0.7	50	17	AZ30749	AZ30749.IM0056J07	799	16.6	0.7	49	9	AA915234
727	16.8	0.7	50	17	TA89E09P	TA89E09P.AL61090.T. brucei	800	16.6	0.7	49	9	AA915234
728	16.8	0.7	50	17	AU010464	AU010464.AU010464	801	16.6	0.7	49	9	AA915234
729	16.8	0.7	50	17	AZ486558	AZ486558.IM0314H12	802	16.6	0.7	49	9	AA915234
730	16.8	0.7	50	17	AA226169	AA226169.nc11g06.t	803	16.6	0.7	49	9	AA915234
731	16.8	0.7	50	17	AA226169	AA226169.nc11g06.t	804	16.6	0.7	49	9	AA915234
732	16.8	0.7	50	17	AA226169	AA226169.nc11g06.t	805	16.6	0.7	49	9	AA915234
733	16.8	0.7	50	17	AA226169	AA226169.nc11g06.t	806	16.6	0.7	49	9	AA915234
734	16.8	0.7	50	17	AA226169	AA226169.nc11g06.t	807	16.6	0.7	49	9	AA915234
735	16.8	0.7	50	17	AA226169	AA226169.nc11g06.t	808	16.6	0.7	49	9	AA915234
736	16.8	0.7	50	17	AA226169	AA226169.nc11g06.t	809	16.6	0.7	49	9	AA915234

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0574 row: P column: 09
Seq primer: CACACAGCAACAGCTGTGACC
Class: plasmid ends
High quality sequence stop: 45.
location/Qualifiers
I. .45
source

Query Match	1.0%;	Score 22.6;	DB 17;	length 45;
Best Local Similarity	75.7%;	Pred. No. 7.6e+05;		
Matches 28;	Conservative 0;	Mismatches 9;	Indels 0;	Gaps 0

QY	1975	ATGCTCACAATTTATTCATTCAATCATTTATTCATT	2011
Db	38	ATAGTCATTCATTCATTCATTCATTCATTCATTCATT	2

RESULT 2					
AZ857401/c		46 bp	DNA	linear	GSS 21-FEB-2001
LOCUS	2M0162M07				
DEFINITION	Mouse 10kb plasmid U0GC11M library Mus musculus genomic				
ACCESSION	clone U0GC2M0162M07 F, DNA sequence.				
VERSION	AZ857401				
KEYWORDS	AZ857401.1 GI:13049443				
SOURCE	GSS.				
	house mouse.				

REFERENCE AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 46), Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M, Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A., and Wright, D., Weiss, R.	Mouse whole genome scaffolding with paired end reads from 10kb Plasmid inserts	Unpublished (2000)	Contact: Robert B. Weiss University of Utah genome center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0162 row: M column: 07
Seq primer: CGTGTAAACGACGCCGACAT
Class: plasmid ends
High quality sequence stop: 46.

FEATURES

source

Location/Qualifiers

1. 46
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U06C2M0162M07"
/clone_11b="Mouse 10kb plasmid U06C1M library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114|9b|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

1 a 23 c 0 g 22 t

ORIGIN

Query Match 1.0%; Score 22; DB 17; Length 46;
Best local Similarity 73.7%; Pred. No. 1.1e+06;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1902 GGCACAGTGGCGAGAGAACAGAAATGATGTA 1939
DB 38 GGGAGAGAGAGTGAAGAGAGAGAGAGAGAGAA 1

RESULT 3
LOCUS A2592788 47 bp DNA linear GSS 13-DEC-2000
DEFINITION M0403P22R Mouse 10kb plasmid U06C1M library Mus musculus genomic
ACCESSION A2592788
VERSION A2592788.1 GI:11714978
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 47)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL COMMENT

plasmid inserts
unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0403 row: P column: 22
Seq primer: CACACAGAAACAGCATATGACC
Class: plasmid ends
High quality sequence stop: 47.

FEATURES

source

Location/Qualifiers

1. 47
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U06C1M0403P22"
/clone_11b="Mouse 10kb plasmid U06C1M library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114|9b|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

12 a 8 c 16 g 11 t

ORIGIN

Query Match 1.0%; Score 22; DB 17; Length 47;
Best local Similarity 67.4%; Pred. No. 1.1e+06;
Matches 31; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1025 CTGAATATTCGAAATTCGAGATTGTAATTCAGAAATG 1070
DB 2 CGTGAAGCGTTGAGATATCTACAGCATTCGAAATTCAGGGCATG 47

RESULT 4
LOCUS A2458729/c 50 bp DNA linear GSS 04-OCT-2000
DEFINITION M0263N06F Mouse 10kb plasmid U06C1M library Mus musculus genomic
ACCESSION A2458729
VERSION A2458729.1 GI:10616854
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 50)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL COMMENT

plasmid inserts
unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah

BASE COUNT	ORIGIN
32 a	4 c 4 g 9 t

RESULT	12
AZ78816/c	
LOCUS	
DEFINITION	AZ788166 Mouse 33 bp DNA linear library Mus musculus genomic
	2M0035P03F
	Mouse 10kb plasmid UNGCJM library Mus musculus genomic

PCR: The PCR products were separated on sequencing gel.
The differential bands were cut, reamplified, cloned into
pMD18-T vector and confirmed by Northern blot."

BASE COUNT

38 a 4 c 0 g 6 t

ORIGIN

Query Match 0.9%; Score 20.4; DB 12; Length 48;
Best Local Similarity 65.2%; Pred. No. 2.7e+06;
Matches 30; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

OY 1104 TGTCTTTGTCGTCGATTTTCAGACTTTTATATGTTAT 1149

Db 46 TTTTGTGTTTGTGTTTGTGTTTAAAGTGTGTTTAAATTTT 1

RESULT 19
AA505166 49 bp mRNA linear EST 18-AUG-1997
LOCUS a646e04.t1 NCI-CGAP-GCB1 Homo sapiens cDNA clone IMAGE:825726 5'
DEFINITION similar to TR:G535513 G535513 HOMOLOG OF YEAST MDTL.; mRNA
sequence.

ACCESSION AA505166

VERSION AA505166.1 GI:2241326

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS 1 (bases 1 to 49)

TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

COMMENT Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,

Ph.D., Gerald Marti, M.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/bdrp/image/image.html

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Seq primer: -28ml3 rev1 ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers

1.49

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:825726"

/clone_lib="NCI-CGAP GCB1"

/tissue_type="germinal center B cell"

/lab_host="DH10B"

/note="Vector: pT73D-Pac (Pharmacia) with a modified

polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA

was prepared from human tonsillar cells enriched for

germinal center B cells by flow sorting (CD20+, IgD-),

provided by Dr. Louis M. Staudt (NCI), Dr. David Allman

(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was

primed with a Not I - oligo(dT) primer

5'-GTGACCAATCTGAGTGGAGCGCCCTCATTTTCTTTTCTTTT-3'

1. Double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not I

and Eco RI sites of the modified pT73 vector. Library

went through one round of normalization, and was

constructed by Bento Soares and M. Fatima Bonaldo."

Query Match 0.9%; Score 20.4; DB 9; Length 49;
Best Local Similarity 71.1%; Pred. No. 2.7e+06;
Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 2067 AATCTGTATAGCTTTAAATATATGACACTTTT 2104

Db 48 AACCTTGTGTTGTCCTTAAATTTATTTTAAGTTT 11

RESULT 20

LOCUS AU104178

DEFINITION AU104178 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone

sequence.

ACCESSION AU104178

VERSION AU104178.1 GI:13553699

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS 1 (bases 1 to 50)

TITLE Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata

, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki

, Y., Nakamura, Y., Suyama, A. and Sugano, S.

Diverse transcriptional initiation revealed by fine, large-scale

mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

JOURNAL 21270072

COMMENT Contact: Yutaka Suzuki

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano

, S. Construction and characterization of a full length-enriched and

a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

Location/Qualifiers

1.50

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="KAT00217"

/clone_lib="Sugano Homo sapiens cDNA library"

/note="Differential display comparison of untreated and

dimethylfumarate treated U937 cells"

BASE COUNT

12 a 18 c 6 g 14 t

ORIGIN

Query Match 0.9%; Score 20.4; DB 9; Length 50;

Best Local Similarity 65.2%; Pred. No. 2.7e+06;

Matches 30; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

OY 1964 AGTAATCAGTATGCTCAACATTTTTCATTCATTCATTATCA 2009

Db 1 AATTAATCAGTATGCTCAACATTTTTCATTCATTCATTATCA 46

RESULT 21

LOCUS AZ617534

DEFINITION AZ617534 50 bp DNA linear GSS 13-DEC-2000

1M0448C22R Mouse 10kb plasmid U00GCM library Mus musculus genomic

clone U00GCM0448C22 R, DNA sequence.

ACCESSION AZ617534

VERSION AZ617534.1 GI:11739724

KEYWORDS GSS.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 50)

Dunn, D., Aoyagi, A., Barber, M., Beccorn, T., Duval, B., Hamill, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly

, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A.

BASE COUNT

24 a 5 c 5 g 15 t

ORIGIN


```
1. 46
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_1ib="NCI-CCAP_K1d5"
/tissue_type="2_pooled tumors (clear cell type)"
lab_host="DH10B"
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Query Match	0.98;	Score 20.2;	DB 9;	Length 46;
Best Local Similarity	75.8%;	Pred. No. 3e+06;		
Matches 25; Conservative	0;	Mismatches 8;	Indels 0;	Gaps 0

RESULT 24
AZ498067

LOCUS	AZ4380b	46 bp	DNA	linear	GSS-05-OCT-2000
DEFINITION	AM3435J12F	Mouse 10kb	Plasmid	UGC1M	Library Mus musculus genomic
ACCESSION	clone UGC1M0335J12 F,	DNA sequence.			
	AZ408067				

VERSION	AZ498067.1	GI:10675583
KEYWORDS	GSS.	
SOURCE	house mouse.	

ORGANISM

REFERENCE
1 (bases 1 to 46)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

mouse whole genome scaffolding with paired end reads from 10K plasmid inserts	mouse whole genome scaffolding with paired end reads from 10K plasmid inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0335 row: 7 column: 12
 Seq primer: CGGCTGTAACGACGCGCCACT
 Class: plasmid ends
 High quality sequence stop: 46.

FEATURES
SOURCE

```

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGGCM035312"
/clone_id="Mouse 10k plasmid UGGCM library"
/sex="male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notes="Vector: pMD4ny. Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

```

(<http://www.jax.org/resources/documents/narseq/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMDA2 (9114732114[9b][AF192072.1], a copy-number inducible derivative of plasmid R1), the vector was linearized with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was ligated to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match	0.98;	Score 20.2;	DB 17;	Length 46;
Best Local Similarity	68.38;	Pred. No. 3e+06;		
Matches 28;	Conservative 0;	Mismatches 13;	Indels 0;	Gaps 0

QY	992	GTCACCTCAATTAATGAATCACATTTTATTGCTCCTGAAT	1032
Db	4	GTCACCTCAATTAATGAATGTGTTCCCTGTTCAAT	44

RESULT 29
A7601365

LOCUS	DEFINITION	Accession	Size	Map	Library	Strategy	Source	Organism	Reference
AZ601365			38 bp		DNA	linear	GSS	13-DEC-2000	
1M0419B07	Mouse 10kb plasmid	U08C1M			library	Mus musculus	genomic		
clone U08C1M0419B07	R ₁ DNA sequence								

ACCESSION	AZ601365	
VERSION	AZ601365.1	GI:11723555
KEYWORDS	GSS.	
SOURCE	house mouse	

SOURCE

REFERENCE	Dunn D Howard A Barber M Peterson E Dunn J
AUTHORS	Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Mus 1 (bases 1 to 38)

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE	DESCRIPTION	FILE NAME
Mouse whole genome scaffolding with paired end reads from 10Kbp plasmid inserts		mouse_scaffolding.plasmid_inserts

JOURNAL Unpublished (2000)
COMMENT Contact: Robert P. Meier

CONTACT: ROBERT B. WEISS
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: dann@genetics.utah.edu
Insert Length: 10000 Std Error: 0.000
Plate: 0419 row: B column: 07
Seq primer: CACACAGAAACACTATGAC
Class: plasmid ends
High quality sequence stop: 38.

FEATURES
SOURCE

```

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U06C1M0419B07"
/clone_lib="Mouse 10kb plasmid U06C1M library"
/sex="Male"
/lab_host="F. Coli strain XL10-gold, T1-resistant, F-"
/note="Vector: pMD4ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

```


1

[illegible]

Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers

FEATURES
Source

1..48 /organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL086K08"
/clone.lib="NIBB Mochii normalized Xenopus tailbud library"
/tissue_type="whole embryo"
/dev_stage="stage 25"
/note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs were oligo-dT primed and directionally cloned. Staging according to Nieuwkoop and Faber. Library is subtracted and was constructed by N. Garrett and A.M. Zorn, (Wellcome/CRC Institute). "

BASE COUNT
ORIGIN

Query Match
Best Local Similarity 60.9%; Pred.No.4.2e+06;
Matches 28; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1091 AAC TTC TCG TGCTG CTGTTC TTGTT C TC CGA ATT T TC AGAG ACT TTT 1136
Db 1 AAATTTTG GGGGG GTTTTT TTTT TTTTGG GGN TTNCN AAAATT TTT 46

RESULT 45
AA835093/c

LOCUS
DEFINITION

AA835093 49 bp mRNA linear EST 23-FEB-1998
AK63B06.s1 Barstead pancreas HPLRBI Homo sapiens cDNA clone
IMAGE:1412531 3' similar to gb:X72781 TRYPSINOGEN IVA PRECURSOR
(HUMAN);, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

AA835093
AA835093.1 GI:2908821
EST.
human.

ORGANISM
REFERENCE
AUTHORS
COMMENT

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 49)
Hallier,L., Allen,M., Bowles,J., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G.P., Marra,M., Martin
White,Y., Wylie,T., Waterston,R. and Wilson,R.
J. Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theisling,B.,
Washington-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (infoimage.llnl.gov) for further information.
Seq primer: -40ml3 fwd. EP from Amersham.

FEATURES
SOURCE

Location/Qualifiers

1..49 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1412531"
/clone.lib="Barstead pancreas HPLRBI"
/sex="female"
/dev_stage="adult, 34 years"
/lab_host="DH10B"
/note="Organ: pancreas; Vector: pTY73D-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoRI; Site_2: NotI;
1st strand cDNA was primed with a Not I - oligo(ct) primer
[5',
TGTTAGCAATCTGAAGGGAGGCCGCCCTTTT TTTT TTTT TTTT TTTT TTTT TTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors

[AATTCGATCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3 vector.
Library constructed by Bob Barstead."

BASE COUNT 12 a 7 c 16 g 14 t

Query Match 0.8%; Score 19.6; DB 9; Length 49;
Best Local Similarity 66.7%; Pred. No. 4.2e+06;
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 142 GTCCCTTCAGTAAGAAGAAAATGTCACATCGATC 183

Db 48 GTCCCTTCAGTCTATACCAATAAGAGCCCTGCTTC 7

RESULT 46
AUI03566/c 50 bp mRNA linear EST 30-AUG-2001

LOCUS AUI03566 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone

DEFINITION HEP17402, mRNA sequence.
AUI03566
AUI03566.1 GI:13553087

KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata

,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki

,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale

mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)

JOURNAL MEDLINE 21270072

COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yusuzuki@ims.u-tokyo.ac.jp
Marryama,K., Suyama,A. and Sugano

,S. Construction and characterization of a full length-enriched and

a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source 1..50
/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="HEP17402"

/note="Differential display comparison of untreated and

dimethylfluminate treated U937 cells"

BASE COUNT 16 a 15 c 9 g 10 t

ORIGIN

Query Match 0.8%; Score 19.6; DB 9; Length 50;
Best Local Similarity 73.5%; Pred. No. 4.2e+06;
Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1455 TTGAGGAGAAAAGCTTAATGATCTGATATGT 1488

Db 44 TTGCGGAGCTAAAGCTAGTGTCTGAGAGCT 11

RESULT 47
AUI03568/c 50 bp mRNA linear EST 30-AUG-2001

LOCUS AUI03568 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone

DEFINITION HEP21445, mRNA sequence.
AUI03568
AUI03568.1 GI:13553089

KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata

,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki

,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale

mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)

JOURNAL MEDLINE 21270072

COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yusuzuki@ims.u-tokyo.ac.jp
Marryama,K., Suyama,A. and Sugano

,S. Construction and characterization of a full length-enriched and

a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source 1..50
/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="HEP21445"

/note="Differential display comparison of untreated and

dimethylfluminate treated U937 cells"

BASE COUNT 13 a 16 c 7 g 14 t

ORIGIN

Query Match 0.8%; Score 19.6; DB 9; Length 50;
Best Local Similarity 73.5%; Pred. No. 4.2e+06;
Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1455 TTGAGGAGAAAAGCTTAATGATCTGATATGT 1488

Db 50 TTGAGGAGCTAAAGCTGTAATTCGAGAGCT 17

RESULT 48
B1175092 50 bp mRNA linear EST 09-JUL-2001

LOCUS B1175092 OSTRO07/H_1 AD-wrmcDNA Caenorhabditis elegans cDNA similar to

F59A2.5, mRNA sequence.
B1175092
B1175092.1 GI:14640895

DEFINITION EST.
Caenorhabditis elegans.

SOURCE Caenorhabditis elegans.

ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Rhabditiodea

1 (bases 1 to 50)
Rhabditiidae; Pelodierinae; Caenorhabditis.

REFERENCE 1 (bases 1 to 50)
Reboul,J., Vaglio,P., Tzelias,N., Thierry-Mieg,N., Moore,T.,

Jackson,C., Shin-I,T., Kohara,Y., Thierry-Mieg,D., Thierry-Mieg,J.,

Lee,H., Hittl,J., Doucet-Stamm,L., Hartley,J.L., Temple,G.F.,

Brasch,M.A., Vandenhauwe,J., Lamesch,P.E., Hill,D.B. and Vidal,M.
Open-reading-frame sequence tags (OSTs) support the existence of at

least 17,300 genes in C. elegans
Nat. Genet. 27 (3), 332-336 (2001)

JOURNAL MEDLINE 21135099

COMMENT Contact: Reboul J, Vaglio P
Marc Vidal Laboratory
Dana Farber Cancer Institute
44 Binney Street, Boston, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 2425

Email: Jerome.Reboul@fci.harvard.edu
Sequence tag of gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFome
cloning project : Contact jerome_reboul@fci.harvard.edu or
philippe_vaglio@fci.harvard.edu
POLYA-NO. Location/Qualifiers
1..50

```

1..50
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U06C2M0214K17"
/clone_lib="Mouse 10kb plasmid U06C2M library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: pCMV2mv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4

```

```

/organism="Zea mays"
/cultivar="mixed background W23/Al88/B73"
/db_xref="taxon:4577"
/clone_lib="1006 - RescueMu Grid G"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/note="organ: leaf; Vector: RescueMu (engineered from
pBluescript backbone); Site: 1: BamHI; Site:2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iasatate.edu' and follow the links for
'RescueMu'. Grid G was grown at Stanford in 2000. DNA was
extracted from leaf punches, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

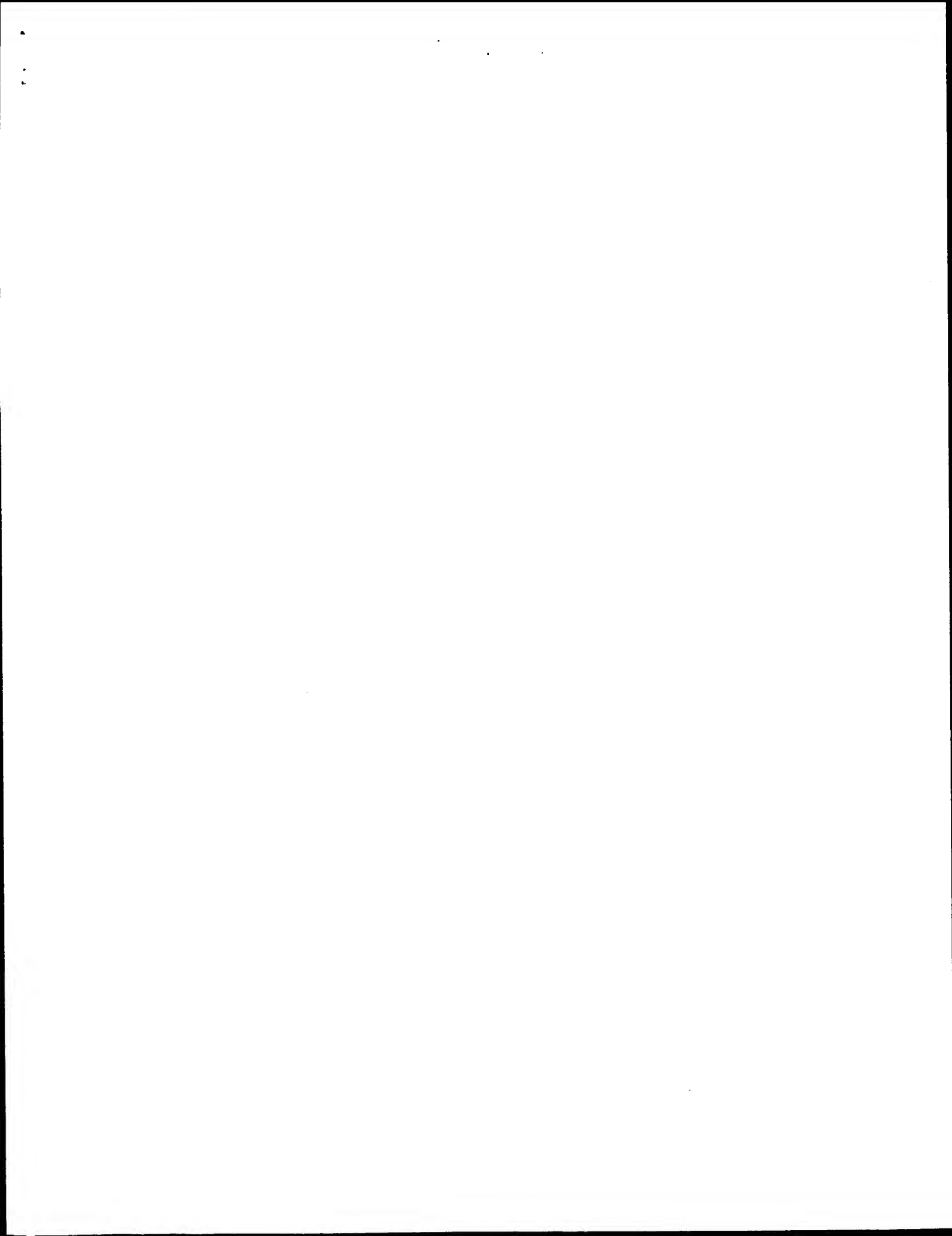
```

BASE COUNT 12 a 15 c 18 g 5 t
ORIGIN

Query Match 0.8%; Score 19.6; DB 17; Length 50;
Best Local Similarity 66.7%; Pred. No. 4.2e+06;
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1884 AGGACCTTGGAGAGCAGGAGGACAGTGTGAGCAGGAGAGAGAAC 1925
DB 9 AGCACCAGAGCCGAGCCAGTGTGAGGAGGAGTGTGTAGATC 50

Search completed: November 11, 2002, 02:35:09
Job time : 2968 secs



GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic : nucleic search, using sw model

Run on: November 10, 2002, 23:22:02 ; Search time 5797 Seconds

(without alignments)
11591.923 Million cell updates/sec

Title: US-09-659-860A-3

Perfect score: 2309

Sequence: 1 ggaagacgtgcagctccca.....gataaaatgtgtgctt 2309

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 841850

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Database : Listing first 1000 summaries

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GenBml:*
1: gb.ba:*
2: gb.htg:*
3: gb.in:*
4: gb.om:*
5: gb.ov:*
6: gb.pat:*
7: gb.ph:*
8: gb.pl:*
9: gb.pr:*
10: gb.ro:*
11: gb.sts:*
12: gb.sy:*
13: gb.un:*
14: gb.vl:*
15: em.ba:*
16: em.fun:*
17: em.hum:*
18: em.in:*
19: em.mu:*
20: em.om:*
21: em.or:*
22: em.ov:*
23: em.pat:*
24: em.ph:*
25: em.pl:*
26: em.ro:*
27: em.sts:*
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32: em.htg.other:*
33: em.htg.mus:*
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35: em.htg.rod:*
36: em.htg.man:*
37: em.htg.vrt:*
38: em.sy:*
39: em.htgo.hum:*
40: em.htgo.mus:*
41: em.htgo.other:*

```

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	1.2	28	6	AR091202 Sequence
2	28	1.2	28	6	AR198237 Sequence
3	27.4	1.2	29	6	AR121773 Sequence
4	27.4	1.2	29	6	AR121774 Sequence
5	27	1.2	27	6	AR091106 Sequence
6	27	1.2	27	6	AR198141 Sequence
7	26	1.1	26	6	AR091105 Sequence
8	26	1.1	26	6	AR091201 Sequence
9	26	1.1	26	6	AR198140 Sequence
10	26	1.1	26	6	AR198236 Sequence
11	25.6	1.1	48	6	AX207739 Sequence
12	25.6	1.1	48	6	AX207745 Sequence
13	23.2	1.0	48	6	AS9018 Sequence 6
14	22.8	1.0	41	6	A66666 Sequence 11
15	22.8	1.0	49	6	AR139393 Sequence
16	22	1.0	50	6	AX159802 Sequence
17	21.8	0.9	37	6	A66667 Sequence 12
18	21.8	0.9	46	6	AS9017 Sequence 5
19	21.8	0.9	47	10	S82867 ApOD-apol1p
20	21.8	0.9	49	6	AR207719 Sequence
21	21.6	0.9	49	6	AS9014 Sequence 2
22	21.4	0.9	45	6	AR124897 Sequence
23	21.4	0.9	48	6	AR134560 Sequence
24	21.2	0.9	47	6	AX094703 Sequence
25	21.2	0.9	48	6	AR153148 Sequence
26	21.2	0.9	48	6	AR210944 Sequence
27	21	0.9	45	6	AS9013 Sequence 1
28	21	0.9	48	12	SYNSYAPLNA
29	21	0.9	50	6	AX159047 Sequence
30	20.8	0.9	43	6	AX484538 Sequence
31	20.8	0.9	49	6	A46759 Sequence 1
32	20.8	0.9	49	6	189340 Sequence 1
33	20.8	0.9	50	6	AX165053 Sequence
34	20.6	0.9	41	6	AR139408 Sequence
35	20.6	0.9	45	6	AR139392 Sequence
36	20.6	0.9	50	6	AX162670 Sequence
37	20.4	0.9	50	6	AX093098 Sequence
38	20.4	0.9	50	6	AX158156 Sequence
39	20.2	0.9	46	10	MMU242789 Mus muscu
40	20.2	0.9	50	6	AX161234 Sequence
41	20.2	0.9	50	6	AX162672 Sequence
42	20.2	0.9	50	6	AX162674 Sequence
43	20.2	0.9	50	6	E22339 DNA encodin
44	20.2	0.9	50	6	E22344 DNA encodin
45	20	0.9	36	6	AR084536 Sequence
46	20	0.9	38	6	AX361209 Sequence
47	20	0.9	39	6	A07129 Nucleotide
48	20	0.9	46	6	E03833 DNA encodin
49	20	0.9	46	6	AR059781 Sequence
50	19.8	0.9	45	6	E60006 Ceramide-bl
51	19.8	0.9	46	6	A98768 Sequence 1
52	19.8	0.9	47	6	AR166259 Sequence
53	19.8	0.9	48	4	AB022055 Canis fam
54	19.8	0.9	50	6	AX160090 Sequence
55	19.6	0.8	33	6	A66668 Sequence 13
56	19.6	0.8	36	6	AX179244 Sequence
57	19.6	0.8	48	6	AX13844 Nucleotide
58	19.6	0.8	49	6	AR093223 Sequence
59	19.4	0.8	35	6	AX061277 Sequence
60	19.4	0.8	35	6	AX061339 Sequence
61	19.4	0.8	36	6	AX061340 Sequence
62	19.4	0.8	37	6	AX061341 Sequence
63	19.4	0.8	38	6	AX061342 Sequence
64	19.4	0.8	38	6	AX223107 Sequence
65	19.4	0.8	39	6	AX061343 Sequence

Pred. No. is the number of results predicted by chance to have a

C 66	19.4	0.8	40	6	AR050327	Sequence	C 139	18.6	0.8	42	6	AR013771	Sequence
C 67	19.4	0.8	40	6	AX061344	Sequence	C 140	18.6	0.8	50	6	AR032855	Sequence
C 68	19.4	0.8	41	6	AX061282	Sequence	C 141	18.6	0.8	50	6	AR032857	Sequence
C 69	19.4	0.8	42	6	AX061283	Sequence	C 142	18.6	0.8	50	6	AR029519	Sequence
C 70	19.4	0.8	43	6	AX061284	Sequence	C 143	18.6	0.8	50	6	AR029521	Sequence
C 71	19.4	0.8	44	6	AX061285	Sequence	C 144	18.6	0.8	50	6	AX190073	Sequence
C 72	19.4	0.8	45	6	AX061286	Sequence	C 145	18.6	0.8	50	6	129595	Sequence
C 73	19.4	0.8	46	6	AX061287	Sequence	C 146	18.6	0.8	50	6	129597	Sequence
C 74	19.4	0.8	47	6	AR211861	Sequence	C 147	18.6	0.8	50	6	191269	Sequence
C 75	19.2	0.8	24	6	AX443237	Sequence	C 148	18.6	0.8	50	6	191271	Sequence
C 76	19.2	0.8	24	6	AX443240	Sequence	C 149	18.6	0.8	50	10	MMU41960	Sequence
C 77	19.2	0.8	24	6	AX443257	Sequence	C 150	18.6	0.8	29	6	MMU41975	Sequence
C 78	19.2	0.8	24	6	AX443260	Sequence	C 151	18.4	0.8	30	6	AX253564	Sequence
C 79	19.2	0.8	35	6	E02802	Sequence	C 152	18.4	0.8	30	6	AX033189	Sequence
C 80	19.2	0.8	36	6	AR105684	Sequence	C 153	18.4	0.8	31	6	AX061335	Sequence
C 81	19.2	0.8	38	6	AX404666	Sequence	C 154	18.4	0.8	32	6	AX061336	Sequence
C 82	19.2	0.8	41	6	AR032234	Sequence	C 155	18.4	0.8	33	6	AX061337	Sequence
C 83	19.2	0.8	41	6	AR201284	Sequence	C 156	18.4	0.8	34	6	AX061338	Sequence
C 84	19.2	0.8	43	9	HUMX	Sequence	C 157	18.4	0.8	34	11	C75760	Sequence
C 85	19.2	0.8	45	6	AR167881	Sequence	C 158	18.4	0.8	36	9	HSTCARB15	Sequence
C 86	19.2	0.8	45	6	AX019802	Sequence	C 159	18.4	0.8	37	6	AX061278	Sequence
C 87	19.2	0.8	48	6	190209	Sequence	C 160	18.4	0.8	38	6	AX061279	Sequence
C 88	19.2	0.8	49	6	AX099434	Sequence	C 161	18.4	0.8	38	6	AX273910	Sequence
C 89	19.2	0.8	49	6	AR148167	Sequence	C 162	18.4	0.8	39	6	AX061280	Sequence
C 90	19.2	0.8	38	6	AX220343	Sequence	C 163	18.4	0.8	40	6	AR160226	Sequence
C 91	19.2	0.8	40	6	AX184221	Sequence	C 164	18.4	0.8	40	6	AR160281	Sequence
C 92	19.2	0.8	41	6	AR109076	Sequence	C 165	18.4	0.8	43	6	108287	Sequence
C 93	19.2	0.8	41	6	AR200731	Sequence	C 166	18.4	0.8	44	6	AX431444	Sequence
C 94	19.2	0.8	45	6	AR168699	Sequence	C 167	18.4	0.8	44	6	E41646	Sequence
C 95	19.2	0.8	45	6	AX027155	Sequence	C 168	18.4	0.8	45	9	HSAN01619	Sequence
C 96	19.2	0.8	45	6	E52000	Sequence	C 169	18.4	0.8	48	4	PIGCFTRB	Sequence
C 97	19.2	0.8	46	5	ELBETAB6	Sequence	C 170	18.4	0.8	49	10	MUSYHCB6	Sequence
C 98	19.2	0.8	46	6	AR163660	Sequence	C 171	18.4	0.8	50	6	A95454	Sequence
C 99	19.2	0.8	46	6	AX259566	Sequence	C 172	18.4	0.8	50	6	AR177517	Sequence
C 100	19.2	0.8	48	9	CALCFTRB	Sequence	C 173	18.4	0.8	50	6	AX147176	Sequence
C 101	19.2	0.8	49	6	AR178011	Sequence	C 174	18.4	0.8	50	6	AX156809	Sequence
C 102	19.2	0.8	49	6	AR178012	Sequence	C 175	18.4	0.8	50	6	AX156811	Sequence
C 103	19.2	0.8	50	6	A39830	Sequence	C 176	18.4	0.8	50	6	AX160546	Sequence
C 104	19.2	0.8	50	6	AR044011	Sequence	C 177	18.4	0.8	50	6	117034	Sequence
C 105	19.2	0.8	50	6	AX158333	Sequence	C 178	18.4	0.8	50	10	MUSRR45SY	Sequence
C 106	19.2	0.8	50	6	AX162190	Sequence	C 179	18.2	0.8	32	6	A63879	Sequence
C 107	19.2	0.8	50	6	AX162668	Sequence	C 180	18.2	0.8	33	6	AR050566	Sequence
C 108	18.8	0.8	31	6	AX203790	Sequence	C 181	18.2	0.8	36	6	124913	Sequence
C 109	18.8	0.8	38	6	AR058162	Sequence	C 182	18.2	0.8	38	6	AX273965	Sequence
C 110	18.8	0.8	38	6	AR115920	Sequence	C 183	18.2	0.8	39	6	182408	Sequence
C 111	18.8	0.8	42	6	AX268903	Sequence	C 184	18.2	0.8	41	6	AR019012	Sequence
C 112	18.8	0.8	42	6	AX268907	Sequence	C 185	18.2	0.8	41	6	AR111609	Sequence
C 113	18.8	0.8	43	6	AX483425	Sequence	C 186	18.2	0.8	41	6	AR147009	Sequence
C 114	18.8	0.8	46	6	E26015	Sequence	C 187	18.2	0.8	41	6	AR158235	Sequence
C 115	18.8	0.8	46	6	T31437	Sequence	C 188	18.2	0.8	42	6	AX006460	Sequence
C 116	18.8	0.8	47	6	AX194723	Sequence	C 189	18.2	0.8	43	6	AX064973	Sequence
C 117	18.8	0.8	48	1	TIP37CG2	Sequence	C 190	18.2	0.8	43	6	AX483385	Sequence
C 118	18.8	0.8	48	6	AR032614	Sequence	C 191	18.2	0.8	43	6	AX484515	Sequence
C 119	18.8	0.8	48	6	AR209278	Sequence	C 192	18.2	0.8	44	6	AX050336	Sequence
C 120	18.8	0.8	48	6	129354	Sequence	C 193	18.2	0.8	45	6	AX100505	Sequence
C 121	18.8	0.8	48	6	T91028	Sequence	C 194	18.2	0.8	48	6	AR146542	Sequence
C 122	18.8	0.8	50	6	A25699	Sequence	C 195	18.2	0.8	48	9	AR202763	Sequence
C 123	18.8	0.8	50	6	AR051358	Sequence	C 196	18.2	0.8	48	9	S6486262	Sequence
C 124	18.8	0.8	50	6	AR059787	Sequence	C 197	18.2	0.8	49	11	S79501	Sequence
C 125	18.8	0.8	50	6	AX158156	Sequence	C 198	18.2	0.8	50	6	AX158915	Sequence
C 126	18.8	0.8	50	6	AX162044	Sequence	C 199	18.2	0.8	50	6	AX160612	Sequence
C 127	18.8	0.8	50	6	AX162044	Sequence	C 200	18.2	0.8	50	6	AX175389	Sequence
C 128	18.8	0.8	50	6	AX162044	Sequence	C 201	18.2	0.8	50	6	AX190280	Sequence
C 129	18.8	0.8	50	6	AX162044	Sequence	C 202	18.2	0.8	50	6	AX204199	Sequence
C 130	18.8	0.8	50	6	E22340	Sequence	C 203	18.2	0.8	34	6	AX406573	Sequence
C 131	18.6	0.8	29	6	AX046883	Sequence	C 204	18.2	0.8	35	6	AR071839	Sequence
C 132	18.6	0.8	35	6	E10813	Sequence	C 205	18.2	0.8	35	6	AR112579	Sequence
C 133	18.6	0.8	39	6	AR202194	Sequence	C 206	18.2	0.8	35	6	AR071839	Sequence
C 134	18.6	0.8	40	6	A20004	Sequence	C 207	18.2	0.8	35	6	174774	Sequence
C 135	18.6	0.8	40	6	AR082637	Sequence	C 208	18.2	0.8	36	6	AR009886	Sequence
C 136	18.6	0.8	40	6	113193	Sequence	C 209	18.2	0.8	36	6	AR023668	Sequence
C 137	18.6	0.8	41	6	AR139391	Sequence	C 210	18.2	0.8	38	6	A73296	Sequence
C 138	18.6	0.8	42	1	CTB23AOMP3	Sequence	C 211	18.2	0.8	38	6	AR061033	Sequence

C 212	18	0.8	38	5	AR161666	Sequence	C 285	17.8	0.8	48	6	I29323	I29323 Sequence 19
C 213	18	0.8	38	5	AX220323	Sequence	C 286	17.8	0.8	48	6	I90997	I90997 Sequence 19
C 214	18	0.8	42	6	AI3916	Nucleotide	C 287	17.8	0.8	49	6	AR023953	AR023953 Sequence
C 215	18	0.8	42	6	AY7032	Sequence 9	C 288	17.8	0.8	49	6	AR205523	AR205523 Sequence
C 216	18	0.8	42	6	AR005061	Sequence	C 289	17.8	0.8	49	6	AX076533	AX076533 Sequence
C 217	18	0.8	42	6	AR060877	Sequence	C 290	17.8	0.8	49	6	AX076540	AX076540 Sequence
C 218	18	0.8	42	6	AR110811	Sequence	C 291	17.8	0.8	49	6	I15454	I15454 Sequence 32
C 219	18	0.8	42	6	I18290	Sequence 36	C 292	17.8	0.8	49	10	MUSIGHSWIT	M26302 Mus musculus
C 220	18	0.8	42	6	I24503	Sequence 34	C 293	17.8	0.8	50	6	AX147188	AX147188 Sequence
C 221	18	0.8	42	6	I28897	Sequence 34	C 294	17.8	0.8	50	10	MTEFAM13	U71389 Mus musculus
C 222	18	0.8	42	6	I33035	Sequence 34	C 295	17.8	0.8	50	12	SYNE17XORE	K00455 chimeric pl
C 223	18	0.8	42	6	I79631	Sequence 34	C 296	17.6	0.8	24	6	AR202878	AR202878 Sequence
C 224	18	0.8	43	6	AR011922	Sequence	C 297	17.6	0.8	25	6	AX050440	AX050440 Sequence
C 225	18	0.8	43	6	AR017793	Sequence	C 298	17.6	0.8	25	6	AX076641	AX076641 Sequence
C 226	18	0.8	43	6	AR077198	Sequence	C 299	17.6	0.8	26	6	AX116990	AX116990 Sequence
C 227	18	0.8	43	6	AX394955	Sequence	C 300	17.6	0.8	28	6	AR094102	AR094102 Sequence
C 228	18	0.8	43	6	AX483555	Sequence	C 301	17.6	0.8	28	6	BD005768	BD005768 Therapeut
C 229	18	0.8	43	6	E38119	DNA elongat	C 302	17.6	0.8	29	6	A66669	A66669 Sequence 14
C 230	18	0.8	45	6	I55013	Sequence 37	C 303	17.6	0.8	34	6	AX358614	AX358614 Sequence
C 231	18	0.8	45	6	I55014	Sequence 38	C 304	17.6	0.8	35	6	A18124	A18124 oligomer de
C 232	18	0.8	46	17	HSMC43F06	X88058 H.sapiens D	C 305	17.6	0.8	35	6	I13227	I13227 Sequence 56
C 233	18	0.8	47	6	I77068	Sequence 10	C 306	17.6	0.8	36	6	AX467364	AX467364 Sequence
C 234	18	0.8	48	6	A76112	Sequence 51	C 307	17.6	0.8	36	6	I33839	I33839 Sequence 33
C 235	18	0.8	50	6	AX108703	Sequence	C 308	17.6	0.8	36	6	A45968	A45968 Sequence 15
C 236	18	0.8	50	6	AX157060	Sequence	C 309	17.6	0.8	38	6	AR048227	AR048227 Sequence
C 237	18	0.8	50	6	AX157272	Sequence	C 310	17.6	0.8	38	6	AX220262	AX220262 Sequence
C 238	18	0.8	50	6	AX158917	Sequence	C 311	17.6	0.8	38	6	AX220293	AX220293 Sequence
C 239	18	0.8	50	14	S44879	(5' end of A	C 312	17.6	0.8	38	6	AX220414	AX220414 Sequence
C 240	17.8	0.8	30	6	AR028268	Sequence	C 313	17.6	0.8	38	6	AX220459	AX220459 Sequence
C 241	17.8	0.8	30	6	AR028269	Sequence	C 314	17.6	0.8	38	6	AX228668	AX228668 Sequence
C 242	17.8	0.8	30	6	AR138672	Sequence	C 315	17.6	0.8	39	6	A66657	A66657 Sequence 2
C 243	17.8	0.8	31	6	A69294	Sequence 33	C 316	17.6	0.8	39	6	I42458	I42458 Sequence 7
C 244	17.8	0.8	31	6	A71971	Sequence 33	C 317	17.6	0.8	39	10	MUSBMP241	D45010 Mouse gene
C 245	17.8	0.8	31	6	AR147159	Sequence	C 318	17.6	0.8	40	6	AR206821	AR206821 Sequence
C 246	17.8	0.8	31	6	BD009847	Avian pol	C 319	17.6	0.8	40	6	AR206823	AR206823 Sequence
C 247	17.8	0.8	32	3	SUPUR7AH	M26279 Sea urchin	C 320	17.6	0.8	40	6	AX001534	AX001534 Sequence
C 248	17.8	0.8	33	6	A47286	Sequence 10	C 321	17.6	0.8	40	6	AX001546	AX001546 Sequence
C 249	17.8	0.8	36	6	AR053365	Sequence	C 322	17.6	0.8	40	6	AX026106	AX026106 Sequence
C 250	17.8	0.8	36	6	AR131089	Sequence	C 323	17.6	0.8	40	6	AX026114	AX026114 Sequence
C 251	17.8	0.8	37	6	AR123484	Sequence	C 324	17.6	0.8	40	6	AX456321	AX456321 Sequence
C 252	17.8	0.8	38	6	A20219	Oligonucleo	C 325	17.6	0.8	40	6	I06599	I06599 Sequence 4
C 253	17.8	0.8	38	6	AR046020	Sequence	C 326	17.6	0.8	41	6	AR003335	AR003335 Sequence
C 254	17.8	0.8	38	6	AR047097	Sequence	C 327	17.6	0.8	41	6	AX078135	AX078135 Sequence
C 255	17.8	0.8	38	6	AX425211	Sequence	C 328	17.6	0.8	41	6	AX343814	AX343814 Sequence
C 256	17.8	0.8	38	6	I53072	Sequence 81	C 329	17.6	0.8	41	6	AX343816	AX343816 Sequence
C 257	17.8	0.8	38	6	I54149	Sequence 18	C 330	17.6	0.8	42	6	AX167628	AX167628 Sequence
C 258	17.8	0.8	39	6	AR009907	Sequence	C 331	17.6	0.8	43	6	AX483529	AX483529 Sequence
C 259	17.8	0.8	39	6	AR110046	Sequence	C 332	17.6	0.8	43	6	AX484544	AX484544 Sequence
C 260	17.8	0.8	39	6	AX047843	Sequence	C 333	17.6	0.8	43	6	E21661	E21661 Spermato
C 261	17.8	0.8	39	6	BD008910	High leve	C 334	17.6	0.8	44	6	AX287944	AX287944 Sequence
C 262	17.8	0.8	39	10	MMBWAHRNA	X60884 M.musculus	C 335	17.6	0.8	44	6	E03020	E03020 DNA encod
C 263	17.8	0.8	40	6	A33232	Synthetic P	C 336	17.6	0.8	45	6	A00699	A00699 Artificial
C 264	17.8	0.8	42	6	AX458217	Sequence	C 337	17.6	0.8	45	6	AR001115	AR001115 Sequence
C 265	17.8	0.8	42	6	AX458218	Sequence	C 338	17.6	0.8	45	6	AR061372	AR061372 Sequence
C 266	17.8	0.8	42	6	BD011209	Human tel	C 339	17.6	0.8	45	6	AR061367	AR061367 Sequence
C 267	17.8	0.8	42	6	E36958	Human telom	C 340	17.6	0.8	45	6	AR088049	AR088049 Sequence
C 268	17.8	0.8	43	6	AX484577	Sequence	C 341	17.6	0.8	45	6	AR108221	AR108221 Sequence
C 269	17.8	0.8	44	6	AX195512	Sequence	C 342	17.6	0.8	45	6	AR108266	AR108266 Sequence
C 270	17.8	0.8	45	6	AR026316	Sequence	C 343	17.6	0.8	45	6	AR148171	AR148171 Sequence
C 271	17.8	0.8	45	6	AR032580	Sequence	C 344	17.6	0.8	45	6	I00379	I00379 Sequence 1
C 272	17.8	0.8	45	6	AR199538	Sequence	C 345	17.6	0.8	45	6	I16178	I16178 Sequence 4
C 273	17.8	0.8	45	6	AR209244	Sequence	C 346	17.6	0.8	45	6	I16223	I16223 Sequence 49
C 274	17.8	0.8	45	6	AX239587	Sequence	C 347	17.6	0.8	45	6	I45552	I45552 Sequence 1
C 275	17.8	0.8	45	6	I29320	Sequence 19	C 348	17.6	0.8	45	6	I45561	I45561 Sequence 10
C 276	17.8	0.8	45	6	I29320	Sequence 19	C 349	17.6	0.8	45	6	I66664	I66664 Sequence 4
C 277	17.8	0.8	46	6	I75984	Sequence 8	C 350	17.6	0.8	45	6	I66709	I66709 Sequence 49
C 278	17.8	0.8	47	6	AR100692	Sequence	C 351	17.6	0.8	45	6	I84758	I84758 Sequence 4
C 279	17.8	0.8	47	6	AR211840	Sequence	C 352	17.6	0.8	45	6	I84603	I84603 Sequence 49
C 280	17.8	0.8	47	9	S75517	Ig S mu/S e	C 353	17.6	0.8	46	6	AX398263	AX398263 Sequence
C 281	17.8	0.8	48	4	BOVCFTRA	M64103 Cow cysti	C 354	17.6	0.8	46	6	A76303	A76303 Sequence 9
C 282	17.8	0.8	48	4	SHPCFTRA	M64104 Sheep cysti	C 355	17.6	0.8	48	6	AR211823	AR211823 Sequence
C 283	17.8	0.8	48	6	AR032583	Sequence	C 356	17.6	0.8	48	6	AX304314	AX304314 Sequence
C 284	17.8	0.8	48	6	AR209247	Sequence	C 357	17.6	0.8	48	10	MUSAOPI506	L41517 Mus musculu

C 358	17.6	0.8	49	6	124205	124205 Sequence 27	431	17.4	0.8	50	6	BD007536	BD007536 Novel con
C 359	17.6	0.8	50	6	AR032859	AR032859 Sequence	432	17.4	0.8	50	9	AF057509	AF057509 Homo sapi
C 360	17.6	0.8	50	6	AR074567	AR074567 Sequence	433	17.2	0.7	24	6	AX443293	AX443293 Sequence
C 361	17.6	0.8	50	6	AR157447	AR157447 Sequence	434	17.2	0.7	27	6	AR029611	AR029611 Sequence
C 362	17.6	0.8	50	6	AR209523	AR209523 Sequence	435	17.2	0.7	27	6	AX317201	AX317201 Sequence
C 363	17.6	0.8	50	6	AX160088	AX160088 Sequence	436	17.2	0.7	29	6	A90854	A90854 Sequence
C 364	17.6	0.8	50	6	AX160212	AX160212 Sequence	437	17.2	0.7	29	6	AX464640	AX464640 Sequence
C 365	17.6	0.8	50	6	AX160924	AX160924 Sequence	438	17.2	0.7	30	6	AX118403	AX118403 Sequence
C 366	17.6	0.8	50	6	AX161238	AX161238 Sequence	439	17.2	0.7	30	6	E41653	E41653 Antibody ag
C 367	17.6	0.8	50	6	AX199542	AX199542 Sequence	440	17.2	0.7	31	6	A92703	A92703 Sequence
C 368	17.6	0.8	50	6	AX233396	AX233396 Sequence	441	17.2	0.7	31	6	AR176183	AR176183 Sequence
C 369	17.6	0.8	50	6	AX441060	AX441060 Sequence	442	17.2	0.7	31	6	AX076626	AX076626 Sequence
C 370	17.6	0.8	50	6	AX485733	AX485733 Sequence	443	17.2	0.7	31	6	AX082570	AX082570 Sequence
C 371	17.6	0.8	50	6	I29599	I29599 Sequence 47	444	17.2	0.7	31	6	AR099242	AR099242 Sequence
C 372	17.6	0.8	50	6	I91273	I91273 Sequence 47	445	17.2	0.7	35	6	AX369210	AX369210 Sequence
C 373	17.6	0.8	50	9	YSCFV1D1	M21990 S.cerevisia	446	17.2	0.7	35	6	AR210413	AR210413 Sequence
C 374	17.6	0.8	50	9	HSTFE1A4	X84968 H.sapiens t	447	17.2	0.7	37	6	AX147670	AX147670 Sequence
C 375	17.6	0.8	50	10	MMU41944	U41944 Mus musculi	448	17.2	0.7	37	6	AX16090	AX16090 Sequence
C 376	17.6	0.8	50	10	MMU41963	AX042792 Sequence	449	17.2	0.7	37	6	E37284	E37284 Process for
C 377	17.6	0.8	25	6	AX004697	AX004697 Sequence	450	17.2	0.7	37	6	E37495	E37495 Process for
C 378	17.4	0.8	29	6	AX236872	AX236872 Sequence	451	17.2	0.7	37	6	E48955	E48955 Process for
C 379	17.4	0.8	29	6	AX236886	AX236886 Sequence	452	17.2	0.7	37	6	I92391	I92391 Sequence
C 380	17.4	0.8	29	6	AX239782	AX239782 Sequence	453	17.2	0.7	37	6	ASNTFRS2	ASNTFRS2 Sequence
C 381	17.4	0.8	29	6	AR093240	AR093240 Sequence	454	17.2	0.7	38	1	AR147037	AR147037 Sequence
C 382	17.4	0.8	30	6	AR101053	AR101053 Sequence	455	17.2	0.7	38	1	AX220372	AX220372 Sequence
C 383	17.4	0.8	30	6	AX057818	AX057818 Sequence	456	17.2	0.7	38	6	AX425390	AX425390 Sequence
C 384	17.4	0.8	35	6	AX050709	AX050709 Sequence	457	17.2	0.7	38	6	A06487	A06487 Nucleotide
C 385	17.4	0.8	35	6	AR050709	AR050709 Sequence	458	17.2	0.7	39	6	AR016773	AR016773 Sequence
C 386	17.4	0.8	36	6	AR093346	AR093346 Sequence	459	17.2	0.7	39	6	A06488	A06488 reverse com
C 387	17.4	0.8	36	6	AR147719	AR147719 Sequence	460	17.2	0.7	39	6	AR081956	AR081956 Sequence
C 388	17.4	0.8	36	6	AR159741	AR159741 Sequence	461	17.2	0.7	39	6	I06513	I06513 Sequence
C 389	17.4	0.8	36	6	AR160433	AR160433 Sequence	462	17.2	0.7	40	6	AR034248	AR034248 Sequence
C 390	17.4	0.8	36	6	AR202389	AR202389 Sequence	463	17.2	0.7	40	6	AR172313	AR172313 Sequence
C 391	17.4	0.8	36	6	AX220342	AX220342 Sequence	464	17.2	0.7	40	6	AX078179	AX078179 Sequence
C 392	17.4	0.8	38	6	AX220360	AX220360 Sequence	465	17.2	0.7	40	6	E58475	E58475 Process for
C 393	17.4	0.8	38	6	AX220514	AX220514 Sequence	466	17.2	0.7	41	6	AX078146	AX078146 Sequence
C 394	17.4	0.8	38	6	AX222310	AX222310 Sequence	467	17.2	0.7	41	6	I52201	I52201 Sequence
C 395	17.4	0.8	38	6	AX223972	AX223972 Sequence	468	17.2	0.7	41	6	AR031676	AR031676 Sequence
C 396	17.4	0.8	38	6	AX425408	AX425408 Sequence	469	17.2	0.7	42	6	AR075444	AR075444 Sequence
C 397	17.4	0.8	39	6	AX377747	AX377747 Sequence	470	17.2	0.7	42	6	AX027286	AX027286 Sequence
C 398	17.4	0.8	40	6	AR184397	AR184397 Sequence	471	17.2	0.7	42	6	AX181200	AX181200 Sequence
C 399	17.4	0.8	42	6	A43626	A43626 Sequence 16	472	17.2	0.7	42	6	I90294	I90294 Sequence
C 400	17.4	0.8	42	6	A84189	A84189 Sequence 14	473	17.2	0.7	42	6	AX084332	AX084332 Sequence
C 401	17.4	0.8	42	6	AR051094	AR051094 Sequence	474	17.2	0.7	43	6	A30410	A30410 Sequence
C 402	17.4	0.8	43	6	A04412	A04412 Oligonucleo	475	17.2	0.7	44	6	AX167841	AX167841 Sequence
C 403	17.4	0.8	43	6	AR200693	AR200693 Sequence	476	17.2	0.7	44	6	A45617	A45617 Sequence
C 404	17.4	0.8	44	6	A94092	A94092 Sequence 73	477	17.2	0.7	45	6	A94953	A94953 Sequence
C 405	17.4	0.8	44	6	AR077611	AR077611 Sequence	478	17.2	0.7	45	6	AX061292	AX061292 Sequence
C 406	17.4	0.8	44	6	AR183291	AR183291 Sequence	479	17.2	0.7	45	6	AR147209	AR147209 Sequence
C 407	17.4	0.8	44	6	AX011177	AX011177 Sequence	480	17.2	0.7	46	6	AR104493	AR104493 Sequence
C 408	17.4	0.8	44	6	AX105035	AX105035 Sequence	481	17.2	0.7	46	6	AX020460	AX020460 Sequence
C 409	17.4	0.8	44	6	AX300148	AX300148 Sequence	482	17.2	0.7	46	6	AX076701	AX076701 Sequence
C 410	17.4	0.8	44	6	I20743	I20743 Sequence 8	483	17.2	0.7	46	6	AX076702	AX076702 Sequence
C 411	17.4	0.8	44	9	S72295S1	S72295 GFla-Platel	484	17.2	0.7	46	6	AX080033	AX080033 Sequence
C 412	17.4	0.8	44	6	AR028906	AR028906 Sequence	485	17.2	0.7	46	6	AX089634	AX089634 Sequence
C 413	17.4	0.8	47	6	AR070123	AR070123 Sequence	486	17.2	0.7	47	6	AX108725	AX108725 Sequence
C 414	17.4	0.8	47	6	AR070311	AR070311 Sequence	487	17.2	0.7	47	6	AX113385	AX113385 Sequence
C 415	17.4	0.8	47	6	AR211466	AR211466 Sequence	488	17.2	0.7	47	6	AX114389	AX114389 Sequence
C 416	17.4	0.8	47	6	AX194757	AX194757 Sequence	489	17.2	0.7	47	6	AX378254	AX378254 Sequence
C 417	17.4	0.8	47	6	AX195039	AX195039 Sequence	490	17.2	0.7	48	1	HIEGCG8	HIEGCG8
C 418	17.4	0.8	47	6	MUSCFTRB	M75125 Mouse cysti	491	17.2	0.7	48	1	A08375	A08375 Oligonucleo
C 419	17.4	0.8	48	10	A92072	A92072 Sequence 13	492	17.2	0.7	48	6		
C 420	17.4	0.8	50	6	A92073	A92073 Sequence 14	493	17.2	0.7	48	6		
C 421	17.4	0.8	50	6	AR148090	AR148090 Sequence	494	17.2	0.7	48	6		
C 422	17.4	0.8	50	6	AX160946	AX160946 Sequence	495	17.2	0.7	48	6		
C 423	17.4	0.8	50	6	AX161236	AX161236 Sequence	496	17.2	0.7	48	6		
C 424	17.4	0.8	50	6	AX162368	AX162368 Sequence	497	17.2	0.7	48	6		
C 425	17.4	0.8	50	6	AX164931	AX164931 Sequence	498	17.2	0.7	48	6		
C 426	17.4	0.8	50	6	AX233377	AX233377 Sequence	499	17.2	0.7	48	6		
C 427	17.4	0.8	50	6	AX316932	AX316932 Sequence	500	17.2	0.7	48	6		
C 428	17.4	0.8	50	6	AX403276	AX403276 Sequence	501	17.2	0.7	48	6		
C 429	17.4	0.8	50	6	BD007535	BD007535 Novel con	502	17.2	0.7	48	6		
C 430	17.4	0.8	50	6			503	17.2	0.7	48	6		

504	17.2	0.7	48	6	150017	150017 Sequence 15	c 577	17	0.7	42	1	CTB24BOMP3	AF070273 Chlamydia
c 505	17.2	0.7	48	10	RNU34914	U34914 Rattus norv	c 578	17	0.7	42	1	CTB2AOMP3	AF070253 Chlamydia
506	17.2	0.7	49	6	AR070482	AR070482 Sequence	c 579	17	0.7	42	1	CTB2BOMP3	AF070261 Chlamydia
507	17.2	0.7	49	6	AX000861	AX000861 Sequence	c 580	17	0.7	42	1	CTB2COMP3	AF070265 Chlamydia
508	17.2	0.7	49	6	I20190	I20190 Sequence 5	c 581	17	0.7	42	1	CTB2DOMP3	AF070269 Chlamydia
509	17.2	0.7	49	6	I43038	I43038 Sequence 21	c 582	17	0.7	42	1	CTB2EOMP3	AF070281 Chlamydia
c 510	17.2	0.7	50	6	AR032732	AR032732 Sequence	c 583	17	0.7	42	1	CTB2FOMP3	AF070285 Chlamydia
c 511	17.2	0.7	50	6	AR032778	AR032778 Sequence	c 584	17	0.7	42	1	CTB2GOMP3	AF070293 Chlamydia
c 512	17.2	0.7	50	6	AR209396	AR209396 Sequence	c 585	17	0.7	42	1	CTB4BOMP3	AF070297 Chlamydia
c 513	17.2	0.7	50	6	AR209442	AR209442 Sequence	c 586	17	0.7	42	1	CTB4COMP3	AF070301 Chlamydia
c 514	17.2	0.7	50	6	AX160388	AX160388 Sequence	c 587	17	0.7	42	1	CTB4DOMP3	AF070305 Chlamydia
c 515	17.2	0.7	50	6	AX160638	AX160638 Sequence	c 588	17	0.7	42	1	CTB6OMP3	AF070323 Chlamydia
c 516	17.2	0.7	50	6	AX164938	AX164938 Sequence	c 589	17	0.7	42	1	CTBREFBOMP3	AF070229 Chlamydia
c 517	17.2	0.7	50	6	AX164939	AX164939 Sequence	c 590	17	0.7	42	6	A12253	A12253 Nucleotide
518	17.2	0.7	50	6	AX430853	AX430853 Sequence	c 591	17	0.7	42	6	A12254	A12254 Nucleotide
c 519	17.2	0.7	50	6	I29472	I29472 Sequence 34	c 592	17	0.7	42	6	A22335	A22335 Primer O-5
c 520	17.2	0.7	50	6	I29518	I29518 Sequence 39	c 593	17	0.7	42	6	AR036048	AR036048 Sequence
c 521	17.2	0.7	50	6	I42242	I42242 Sequence 55	c 594	17	0.7	42	6	AR071819	AR071819 Sequence
c 522	17.2	0.7	50	6	I42243	I42243 Sequence 56	c 595	17	0.7	42	6	AR112559	AR112559 Sequence
c 523	17.2	0.7	50	6	I91146	I91146 Sequence 34	c 596	17	0.7	42	6	AR112635	AR112635 Sequence
c 524	17.2	0.7	50	6	I91192	I91192 Sequence 39	c 597	17	0.7	42	6	AX079214	AX079214 Sequence
c 525	17.2	0.7	50	9	AF057516	AF057516 Homo sapi	c 598	17	0.7	42	6	AX080047	AX080047 Sequence
c 526	17.2	0.7	50	10	MM041965	U41965 Mus musculu	c 599	17	0.7	42	6	AX080057	AX080057 Sequence
527	17	0.7	30	6	AR084918	AR084918 Sequence	c 600	17	0.7	42	6	E12872	E12872 Primer 4/1
c 528	17	0.7	30	6	AR204083	AR204083 Sequence	c 601	17	0.7	42	6	E35712	E35712 Method for
c 529	17	0.7	30	6	AX024999	AX024999 Sequence	c 602	17	0.7	42	6	I14320	I14320 Sequence 18
c 530	17	0.7	30	6	AX282528	AX282528 Sequence	c 603	17	0.7	42	6	I85726	I85726 Sequence 75
c 531	17	0.7	30	6	E50447	E50447 Odoriferus	c 604	17	0.7	42	11	AL773259	AL773259 Arabidops
c 532	17	0.7	33	6	AR079765	AR079765 Sequence	c 605	17	0.7	43	6	A05113	A05113 Oligonucleo
c 533	17	0.7	33	6	AR081295	AR081295 Sequence	c 606	17	0.7	43	6	AX483499	AX483499 Sequence
c 534	17	0.7	33	6	AR170655	AR170655 Sequence	c 607	17	0.7	43	6	AX484397	AX484397 Sequence
c 535	17	0.7	34	6	AR012331	AR012331 Sequence	c 608	17	0.7	43	6	AX484537	AX484537 Sequence
c 536	17	0.7	34	6	AR012334	AR012334 Sequence	c 609	17	0.7	43	6	AX484545	AX484545 Sequence
c 537	17	0.7	34	6	AR111892	AR111892 Sequence	c 610	17	0.7	44	6	AR110224	AR110224 Sequence
c 538	17	0.7	34	6	AR142228	AR142228 Sequence	c 611	17	0.7	44	6	AR110237	AR110237 Sequence
c 539	17	0.7	35	6	AR095225	AR095225 Sequence	c 612	17	0.7	44	6	AR168983	AR168983 Sequence
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c 543	17	0.7	36	6	AR033955	AR033955 Sequence	c 616	17	0.7	44	6	BD009017	BD009017 Promoter
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c 545	17	0.7	36	6	AX032536	AX032536 Sequence	c 618	17	0.7	45	6	A05540	A05540 Oligonucleo
c 546	17	0.7	36	6	AX236831	AX236831 Sequence	c 619	17	0.7	45	6	AR09110	AR09110 Sequence 5
c 547	17	0.7	36	6	AX298175	AX298175 Sequence	c 620	17	0.7	45	6	AR091633	AR091633 Sequence
c 548	17	0.7	38	6	AR011526	AR011526 Sequence	c 621	17	0.7	45	6	AR066029	AR066029 Sequence
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c 551	17	0.7	38	6	AX220350	AX220350 Sequence	c 624	17	0.7	45	6	AR205027	AR205027 Sequence
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c 553	17	0.7	38	6	AX220431	AX220431 Sequence	c 626	17	0.7	45	6	AX027580	AX027580 Sequence
c 554	17	0.7	38	6	AX228647	AX228647 Sequence	c 627	17	0.7	45	6	AX074248	AX074248 Sequence
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c 556	17	0.7	38	6	AX273554	AX273554 Sequence	c 629	17	0.7	45	6	AX370653	AX370653 Sequence
c 557	17	0.7	38	6	AX273891	AX273891 Sequence	c 630	17	0.7	45	6	AX377734	AX377734 Sequence
c 558	17	0.7	38	6	AX274016	AX274016 Sequence	c 631	17	0.7	45	6	AX477478	AX477478 Sequence
c 559	17	0.7	38	6	AX425412	AX425412 Sequence	c 632	17	0.7	45	6	BD010483	BD010483 Agents fo
c 560	17	0.7	38	6	E11257	E11257 PCR primer	c 633	17	0.7	45	6	I09090	I09090 Sequence 9
c 561	17	0.7	39	6	I18164	I18164 Sequence 40	c 634	17	0.7	45	6	I28424	I28424 Sequence 5
c 562	17	0.7	39	6	AR128128	AR128128 Sequence	c 635	17	0.7	45	10	RATMLV5	M23125 Rat provide
c 563	17	0.7	39	6	AR164496	AR164496 Sequence	c 636	17	0.7	46	6	AR032675	AR032675 Sequence
c 564	17	0.7	39	6	AX081623	AX081623 Sequence	c 637	17	0.7	46	6	AR122827	AR122827 Sequence
c 565	17	0.7	39	6	AX374804	AX374804 Sequence	c 638	17	0.7	46	6	AR131221	AR131221 Sequence
c 566	17	0.7	39	6	AX461676	AX461676 Sequence	c 639	17	0.7	46	6	AR209339	AR209339 Sequence
c 567	17	0.7	40	6	HS010897	HS010897 Homo sapi	c 640	17	0.7	46	6	I29415	I29415 Sequence 28
c 568	17	0.7	41	6	AX035990	AX035990 Sequence	c 641	17	0.7	46	6	I91089	I91089 Sequence 28
c 569	17	0.7	41	6	AR182108	AR182108 Sequence	c 642	17	0.7	47	6	AR079493	AR079493 Sequence
c 570	17	0.7	41	6	I07162	I07162 Sequence 4	c 643	17	0.7	47	6	AX194747	AX194747 Sequence
c 571	17	0.7	42	1	AF178265S3	AF178267 Chlamydia	c 644	17	0.7	47	6	AX378277	AX378277 Sequence
c 572	17	0.7	42	1	AF178269S3	AF178271 Chlamydia	c 645	17	0.7	47	6	AX378277	AX378277 Sequence
c 573	17	0.7	42	1	AF178273S3	AF178275 Chlamydia	c 646	17	0.7	48	1	AX378506	AX378506 Sequence
c 574	17	0.7	42	1	CTB124AOMP3	AF070249 Chlamydia	c 647	17	0.7	48	6	ti1p37CG2	J01824 Integrated
c 575	17	0.7	42	1	CTB12AOMP3	AF070241 Chlamydia	c 648	17	0.7	48	6	A22117	A22117 thrombin an
c 576	17	0.7	42	1	CTB24AOMP3	AF070257 Chlamydia	c 649	17	0.7	48	6	I45633	I45633 Sequence 21

650	17	0.7	48	6	I45634	145634 Sequence 23	723	16.8	0.7	36	6	AX000359	AX000359 Sequence
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652	17	0.7	48	17	HSCHO6F06	X88550 H.sapiens D	C 725	16.8	0.7	36	6	I26097	I26097 Sequence 23
653	17	0.7	49	6	AB3844	AB3844 Sequence 3	C 726	16.8	0.7	36	6	I36091	I36091 Sequence 41
654	17	0.7	49	6	AR011234	AR011234 Sequence	C 727	16.8	0.7	37	6	AR139390	AR139390 Sequence
655	17	0.7	49	6	AR011235	AR011235 Sequence	C 728	16.8	0.7	37	6	AR047325	AR047325 Sequence
656	17	0.7	49	6	AR093225	AR093225 Sequence	C 729	16.8	0.7	38	6	AX129023	AX129023 Sequence
657	17	0.7	49	6	AR146538	AR146538 Sequence	C 730	16.8	0.7	38	6	AX220295	AX220295 Sequence
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659	17	0.7	49	6	I17873	I17873 Sequence 10	C 732	16.8	0.7	38	6	AX425304	AX425304 Sequence
660	17	0.7	49	6	I42247	I42247 Sequence 60	C 733	16.8	0.7	38	6	AX425357	AX425357 Sequence
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662	17	0.7	50	6	A02843	A02843 Artificial	C 735	16.8	0.7	38	6	BD012638	BD012638 Human cyt
663	17	0.7	50	6	A12059	A12059 Oligonucleo	C 736	16.8	0.7	38	6	I54377	I54377 Sequence 21
664	17	0.7	50	6	A25699	A25699 MOVHLINK3 p	C 737	16.8	0.7	38	23	BD008206	BD008206 Human cyt
665	17	0.7	50	6	AR032771	AR032771 Sequence	C 738	16.8	0.7	39	6	AR001557	AR001557 Sequence
666	17	0.7	50	6	AR032856	AR032856 Sequence	C 739	16.8	0.7	39	6	AR093715	AR093715 Sequence
667	17	0.7	50	6	AR051358	AR051358 Sequence	C 740	16.8	0.7	39	6	AR139643	AR139643 Sequence
668	17	0.7	50	6	AR209435	AR209435 Sequence	C 741	16.8	0.7	39	6	AR165977	AR165977 Sequence
669	17	0.7	50	6	AR209520	AR209520 Sequence	C 742	16.8	0.7	39	6	AR182871	AR182871 Sequence
670	17	0.7	50	6	AX079226	AX079226 Sequence	C 743	16.8	0.7	39	6	AX000902	AX000902 Sequence
671	17	0.7	50	6	AX080068	AX080068 Sequence	C 744	16.8	0.7	39	6	E11258	E11258 PCR primer
672	17	0.7	50	6	AX127337	AX127337 Sequence	C 745	16.8	0.7	39	6	E60089	E60089 Endonucleas
673	17	0.7	50	6	AX162041	AX162041 Sequence	C 746	16.8	0.7	40	6	A65366	A65366 Sequence 2
674	17	0.7	50	6	AX162710	AX162710 Sequence	C 747	16.8	0.7	40	6	AR100922	AR100922 Sequence
675	17	0.7	50	6	AX190222	AX190222 Sequence	C 748	16.8	0.7	40	6	AX136807	AX136807 Sequence
676	17	0.7	50	6	AX199704	AX199704 Sequence	C 749	16.8	0.7	40	6	AX456219	AX456219 Sequence
677	17	0.7	50	6	E50448	E50448 Odoriferous	C 750	16.8	0.7	40	6	E11812	E11812 Synthetic r
678	17	0.7	50	6	I29511	I29511 Sequence 38	C 751	16.8	0.7	40	6	E55311	E55311 Linkage at
679	17	0.7	50	6	I29596	I29596 Sequence 46	C 752	16.8	0.7	40	6	E64594	E64594 Immobilizat
680	17	0.7	50	6	I91185	I91185 Sequence 38	C 753	16.8	0.7	40	6	E64600	E64600 Immobilizat
681	17	0.7	50	6	I91270	I91270 Sequence 46	C 754	16.8	0.7	40	6	AX059989	AX059989 Sequence
682	17	0.7	50	6	I91270	I91270 Sequence 46	C 755	16.8	0.7	41	6	AX059989	AX059989 Sequence
683	17	0.7	50	10	AF357428	AF357428 Mus muscu	C 756	16.8	0.7	41	6	AX128530	AX128530 Sequence
684	16.8	0.7	25	6	AX139465	AX139465 Sequence	C 757	16.8	0.7	41	6	AX128531	AX128531 Sequence
685	16.8	0.7	28	6	AX033186	AX033186 Sequence	C 758	16.8	0.7	41	6	AX303601	AX303601 Sequence
686	16.8	0.7	30	6	AR028237	AR028237 Sequence	C 759	16.8	0.7	41	6	AX327077	AX327077 Sequence
687	16.8	0.7	30	6	AR138640	AR138640 Sequence	C 760	16.8	0.7	41	6	I12934	I12934 Sequence 14
688	16.8	0.7	31	6	AR7137	AR7137 Sequence 47	C 761	16.8	0.7	41	6	I12935	I12935 Sequence 15
689	16.8	0.7	31	6	AR7180	AR7180 Sequence 15	C 762	16.8	0.7	42	6	AR82218	AR82218 Sequence 39
690	16.8	0.7	31	6	AR053308	AR053308 Sequence	C 763	16.8	0.7	42	6	AR061602	AR061602 Sequence
691	16.8	0.7	31	6	AR157880	AR157880 Sequence	C 764	16.8	0.7	42	6	AR108501	AR108501 Sequence
692	16.8	0.7	31	6	AR206391	AR206391 Sequence	C 765	16.8	0.7	42	6	BD007247	BD007247 Novel flt
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702	16.8	0.7	33	6	AX428309	AX428309 Sequence	C 775	16.8	0.7	43	6	AR050868	AR050868 Sequence
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C 804	16.8	0.7	46	6	AX225288	AX225288 Sequence	C 877	16.6	0.7	35	11	C75873	C75873 Homo sapien
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C 830	16.8	0.7	50	6	AX157664	AX157664 Sequence	C 903	16.6	0.7	39	6	182409	182409 Sequence 60
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C 994	16.6	0.7	50	9	AF098331	Homo sapi
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ALIGNMENTS

RESULT 1
LOCUS AR091202/c
DEFINITION Sequence 1322 from patent US 5994076.
ACCESSION AR091202
VERSION AR091202.1 GI:10017957
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

28 bp DNA
linear PAT 07-SEP-2000

REFERENCE 1 (bases 1 to 28)
AUTHORS Chenchik, A., Jorkhadze, G. and Bibilashvili, R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 5994076-A 1322 30-NOV-1999;
FEATURES
source location/Qualifiers
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BASE COUNT 8 a 5 c 9 g 6 t
ORIGIN

Query Match 1.2%; Score 28; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.4e+04;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 859 CTTGAGTCTCAGTCTGATGACCCACAC 886
Db 28 CTTGAGTCTCAGTCTGATGACCCACAC 1

RESULT 2
LOCUS AR198237/c
DEFINITION Sequence 1322 from patent US 6352829.
ACCESSION AR198237
VERSION AR198237.1 GI:20248086
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Chenchik, A., Jorkhadze, G. and Bibilashvili, R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6352829-A 1322 05-MAR-2002;
FEATURES
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Best Local Similarity 100.0%; Pred. No. 5.4e+04;
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Db 28 CTTGAGTCTCAGTCTGATGACCCACAC 1

RESULT 3
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DEFINITION Sequence 37 from patent US 6160095.
ACCESSION AR121773
VERSION AR121773.1 GI:14105349
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 29)
AUTHORS Chaudhary, P. M. and Hood, L.
TITLE Proteins capable of regulating NF- κ B, JNK and apoptosis
pathways and methods of using the same
JOURNAL Patent: US 6160095-A 37 12-DEC-2000;
FEATURES
source location/Qualifiers
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Best Local Similarity 96.6%; Pred. No. 7.5e+04;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 TCTTCATTGAGGCTAGCCGAGGAGACCGAG 29

RESULT 4
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LOCUS ARI21774 29 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 38 from patent US 6160095.
ACCESSION ARI21774
VERSION ARI21774.1 GI:14105350
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 29)
AUTHORS Chaudhary,P.M. and Hood,L.
TITLE Proteins capable of regulating NF-kappa,B, JNK and apoptosis
pathways and methods of using the same
JOURNAL Patent: US 6160095-A 38 12-DEC-2000;
FEATURES
Source Location/Qualifiers
1..29
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BASE COUNT 6 a 9 c 8 g 6 t
ORIGIN

Query Match 1.2%; Score 27.4; DB 6; Length 29;
Best Local Similarity 96.6%; Pred. No. 7.5e+04;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 585 TCTTCATTGAGGCTGGCCGAGACCGAG 613
Db 29 TCTTCATTGAGGCTAGCCGAGGAGACCGAG 1

RESULT 5
AR091106/c
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DEFINITION Sequence 1226 from patent US 5994076.
ACCESSION AR091106
VERSION AR091106.1 GI:10017861
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 27)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvili,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 5994076-A 1226 30-NOV-1999;
FEATURES
Source Location/Qualifiers
1..27
/organism="unknown"

BASE COUNT 9 a 1 c 13 g 4 t
ORIGIN

Query Match 1.2%; Score 27; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1812 TCTCACCCTATCTGCGCTGCACATCTTC 1838
Db 27 TCTCACCCTATCTGCGCTGCACATCTTC 1

RESULT 6
ARI98141/c
LOCUS ARI98141 27 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1226 from patent US 6352829.
ACCESSION ARI98141
VERSION ARI98141.1 GI:20247990
KEYWORDS
SOURCE Unknown.

Query Match 1.1%; Score 26; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 27)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvili,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 6352829-A 1226 05-MAR-2002;
FEATURES
Source Location/Qualifiers
1..27
/organism="unknown"

BASE COUNT 9 a 1 c 13 g 4 t
ORIGIN

Query Match 1.2%; Score 27; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 9.4e+04;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1812 TCTCACCCTATCTGCGCTGCACATCTTC 1838
Db 27 TCTCACCCTATCTGCGCTGCACATCTTC 1

RESULT 7
AR091105
LOCUS AR091105 26 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 1225 from patent US 5994076.
ACCESSION AR091105
VERSION AR091105.1 GI:10017860
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 26)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvili,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 5994076-A 1225 30-NOV-1999;
FEATURES
Source Location/Qualifiers
1..26
/organism="unknown"

BASE COUNT 7 a 7 c 7 g 5 t
ORIGIN

Query Match 1.1%; Score 26; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1605 TGTTCACACACCGAGGCTATGAGGA 1630
Db 1 TGTTCACACACCGAGGCTATGAGGA 26

RESULT 8
AR091201
LOCUS AR091201 26 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 1321 from patent US 5994076.
ACCESSION AR091201
VERSION AR091201.1 GI:10017956
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 26)
AUTHORS Chenchik,A., Jokhadze,G. and Bibilashvili,R.
TITLE Methods of assaying differential expression
JOURNAL Patent: US 5994076-A 1321 30-NOV-1999;
FEATURES
Source Location/Qualifiers
1..26
/organism="unknown"

BASE COUNT 4 a 7 c 7 g 8 t
ORIGIN

Query Match 1.1%; Score 26; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 584 TTCTTCATTCAGGCTTGCGAGGAGC 609
 DB 1 TTCTTCATTCAGGCTTGCGAGGAGC 26

RESULT 9
 AR198140
 LOCUS AR198140 26 bp DNA linear PAT 20-APR-2002
 DEFINITION Sequence 1225 from patent US 6352829.
 ACCESSION AR198140
 VERSION AR198140.1 GI:20247989
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 26)
 AUTHORS Chenchik,A., Johhadze,G. and Bibilashvili,I.R.
 TITLE Methods of assaying differential expression
 JOURNAL Patent: US 6352829-A 1225 05-MAR-2002;
 FEATURES Location/Qualifiers
 source 1..26
 /organism="unknown"

BASE COUNT 7 a 7 c 7 g 5 t

Query Match 1.1%; Score 26; DB 6; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.6e+05;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1605 TGTTACACACCCAGGCTATGAGA 1630
 DB 1 TGTTACACACCCAGGCTATGAGA 26

RESULT 10
 AR198236
 LOCUS AR198236 26 bp DNA linear PAT 20-APR-2002
 DEFINITION Sequence 1321 from patent US 6352829.
 ACCESSION AR198236
 VERSION AR198236.1 GI:20248085
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 26)
 AUTHORS Chenchik,A., Johhadze,G. and Bibilashvili,I.R.
 TITLE Methods of assaying differential expression
 JOURNAL Patent: US 6352829-A 1321 05-MAR-2002;
 FEATURES Location/Qualifiers
 source 1..26
 /organism="unknown"

BASE COUNT 4 a 7 c 7 g 8 t

Query Match 1.1%; Score 26; DB 6; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.6e+05;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 584 TTCTTCATTCAGGCTTGCGAGGAGC 609
 DB 1 TTCTTCATTCAGGCTTGCGAGGAGC 26

RESULT 11
 AX207739/c 48 bp DNA linear PAT 31-AUG-2001
 LOCUS AX207739/c 48 bp DNA linear PAT 31-AUG-2001
 DEFINITION Sequence 37 from Patent WO0157242.
 ACCESSION AX207739
 VERSION AX207739.1 GI:15422423
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct

artificial sequences.
 1 (bases 1 to 48)
 AUTHORS Stack,J.H., Whitney,M., Cubitt,A.B. and Pollok,B.A.
 TITLE Methods of protein destabilization and uses thereof
 JOURNAL Patent: WO 0157242-A 37 09-AUG-2001;
 Aurora Biosciences Corporation (US)
 FEATURES Location/Qualifiers
 source 1..48
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="Primer for PCR"

BASE COUNT 17 a 7 c 11 g 13 t

Query Match 1.1%; Score 25.6; DB 6; Length 48;
 Best Local Similarity 77.5%; Pred. No. 2.1e+05;
 Matches 31; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 912 GTGTGTCCTCCATGCTCACCAAGAACTCTACTTCAGTCA 951
 DB 48 GTATGTTTCATGCTCTCACAAAGAACTCTATTATTATCA 9

RESULT 12
 AX207745/c 48 bp DNA linear PAT 31-AUG-2001
 LOCUS AX207745/c 48 bp DNA linear PAT 31-AUG-2001
 DEFINITION Sequence 43 from Patent WO0157242.
 ACCESSION AX207745
 VERSION AX207745.1 GI:15422429
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 48)
 AUTHORS Stack,J.H., Whitney,M., Cubitt,A.B. and Pollok,B.A.
 TITLE Methods of protein destabilization and uses thereof
 JOURNAL Patent: WO 0157242-A 43 09-AUG-2001;
 Aurora Biosciences Corporation (US)
 FEATURES Location/Qualifiers
 source 1..48
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="Primer for PCR"

BASE COUNT 17 a 7 c 11 g 13 t

Query Match 1.1%; Score 25.6; DB 6; Length 48;
 Best Local Similarity 77.5%; Pred. No. 2.1e+05;
 Matches 31; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 912 GTGTGTCCTCCATGCTCACCAAGAACTCTACTTCAGTCA 951
 DB 48 GTATGTTTCATGCTCTCACAAAGAACTCTATTATTATCA 9

RESULT 13
 A59018 48 bp DNA linear PAT 06-MAR-1998
 LOCUS A59018 48 bp DNA linear PAT 06-MAR-1998
 DEFINITION Sequence 6 from Patent EP0753581.
 ACCESSION A59018
 VERSION A59018.1 GI:3714453
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unclassified.

REFERENCE 1 (bases 1 to 48)
 AUTHORS Schefflinger,F.D., Antoine,G.D., Falkner, Falco-Guenter,D.,
 Dornier,F.P. and Elbl,J.D.
 TITLE Improved recombinant eukaryotic cytoplasmic viruses, method for
 their production and their use as vaccines
 JOURNAL Patent: EP 0753581-A 6 15-JAN-1997;
 IMMUNO AG (AT)
 FEATURES Location/Qualifiers

source 1. 48
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 17 a 6 c 4 g 21 t

Query Match 1.0%; Score 23.2; DB 6; Length 48;
Best Local Similarity 70.5%; Pred. No. 8.2e+05;
Matches 31; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2060 ATGTGCAATCTGTATAGCTTTAAATATATCTGGAACCTTT 2103
Db 2 ATCTGTTAACTTATTTATAGCATAGAAATATATTTCACCTTT 45

RESULT 14
LOCUS A66666 41 bp DNA linear PAT 29-MAR-1999
DEFINITION Sequence 11 from Patent WO9740172.
ACCESSION A66666
VERSION A66666.1 GI:4538156
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 41)
AUTHORS Mallet,J., Meloni,R., Ravassard,P. and Treilhou,F.
TITLE DERIVED TYROSINE HYDROXYLASE GENE EXPRESSION SYSTEM
JOURNAL Patent: WO 9740172-A 11 30-OCT-1997;
COMMENT RHONE-POULENC ROGER SA (FR)
FEATURES
source Location/Qualifiers
BASE COUNT 9 a 14 c 0 g 18 t

Query Match 1.0%; Score 22.8; DB 6; Length 41;
Best Local Similarity 79.4%; Pred. No. 1e+06;
Matches 27; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1978 CTCACAAATTTATCATTCATTCATTTATTCATT 2011
Db 3 CTCATTCATTCATTCATTCATTCATTCATTCATT 36

RESULT 15
LOCUS ARI39393 49 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 6 from patent US 6207373.
ACCESSION ARI39393
VERSION ARI39393.1 GI:14481889
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 49)
AUTHORS Sosnowski,R.G. and Tu,E.
TITLE Methods for determining nature of repeat units in DNA
JOURNAL Patent: US 6207373-A 6 27-MAR-2001;
FEATURES
source Location/Qualifiers
BASE COUNT 9 a 16 c 0 g 24 t

Query Match 1.0%; Score 22.8; DB 6; Length 49;
Best Local Similarity 79.4%; Pred. No. 1e+06;
Matches 27; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1978 CTCACAAATTTATCATTCATTCATTTATTCATT 2011
Db 3 CTCATTCATTCATTCATTCATTCATTCATTCATT 36

Db 16 CTCATTCATTCATTCATTCATTCATTCATTCATT 49

RESULT 16
LOCUS AX159802/c 50 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 3130 from Patent WO0140521.
ACCESSION AX159802
VERSION AX159802.1 GI:14541133
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
JOURNAL methods of use thereof
Patent: WO 0140521-A 3130 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
misc_feature 1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
misc_feature 25..26
/note="Nucleotide deleted between bases 25 and 26
Accession number cg42922107"
BASE COUNT 9 a 21 c 11 g 9 t

Query Match 1.0%; Score 22; DB 6; Length 50;
Best Local Similarity 67.4%; Pred. No. 1.6e+06;
Matches 31; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1473 AATGATTCGTATATGTATCATTCAGATCCAGTCGTGAAACAGAA 1518
Db 48 ACTGTAAGTGTGTCTGTGCGTCGAGATCCAGGTGACAGACAGAGA 3

RESULT 17
LOCUS A66667 37 bp DNA linear PAT 29-MAR-1999
DEFINITION Sequence 12 from Patent WO9740172.
ACCESSION A66667
VERSION A66667.1 GI:4538157
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 37)
AUTHORS Mallet,J., Meloni,R., Ravassard,P. and Treilhou,F.
TITLE DERIVED TYROSINE HYDROXYLASE GENE EXPRESSION SYSTEM
JOURNAL Patent: WO 9740172-A 12 30-OCT-1997;
COMMENT RHONE-POULENC ROGER SA (FR)
FEATURES
source Location/Qualifiers
BASE COUNT 8 a 13 c 0 g 16 t

Query Match 0.9%; Score 21.8; DB 6; Length 37;
Best Local Similarity 78.8%; Pred. No. 1.8e+06;
Matches 26; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1978 CTCACAAATTTATCATTCATTCATTTATTCATT 2010
Db 3 CTCATTCATTCATTCATTCATTCATTCATTCATT 35

[illegible]

	Query Match	0.9%;	Score 21.8;	DB 10;	Length 47;	
	Best Local Similarity	78.8%;	Pred. No. 1.8e+06;			
Matches	26;	Conservative	0;	Mismatches	7;	Indels
						Gaps
						0
Qy	1850 TACTGCCAGGCTATCTGGAGCCACCTCAC	1882				
Dd	1 TTCTCCCGAGGCCTCTCTGCAAGCACCACC	33				
RESULT 20						
LOCUS	AR207719	49 bp	DNA	linear	PAT 20-JUN-2002	
DEFINITION	Sequence 59 from patent US 6379897.					
ACCESSION	AR207719					
VERSION	AR207719.1	GI:21507547				
KEYWORDS	.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 49)					
AUTHORS	Weidenhammer,E.M., Wang,L., Xu,X., Heller,M.J. and Kahl,B.F.					
TITLE	Methods for gene expression monitoring on electronic microarrays					
JOURNAL	Patent: US 6379897-A 59-30-APR-2002;					
FEATURES	Location/Qualifiers					
source	1..49 /organism="unknown"					
BASE COUNT	20 a 5 c 12 g 12 t					
ORIGIN						
Query Match	0.9%;	Score 21.8;	DB 6;	Length 49;		
Best Local Similarity	70.7%;	Pred. No. 1.8e+06;				
Matches	29;	Conservative	0;	Mismatches	12;	Indels
						Gaps
						0;
Qy	1979 TCACAATTTCATTCATCATTTATTCATTTGGGTTC	2019				
Dd	46 TCATTCATTCATTCATTCATTCATTCATTCATTCAGTGAAGGCTC	6				
RESULT 21						
LOCUS	A59014	49 bp	DNA	linear	PAT 06-MAR-1998	
DEFINITION	Sequence 2 from Patent EP0753581.					
ACCESSION	A59014					
VERSION	A59014.1	GI:3714449				
KEYWORDS	.					
SOURCE	unidentified.					
ORGANISM	unclassified.					
REFERENCE	1 (bases 1 to 49)					
AUTHORS	Scheiflinger,F.P., Antoine,G.D., Falkner, Falco-Guentler,D., Dorner,F.B. and Eibl,J.D. Improved recombinant eukaryotic cytoplasmic viruses, method for their production and their use as vaccines Patent: EP 0753581-A 2 15-JAN-1997; IMMUNO AG (AT)					
TITLE	Location/Qualifiers					
JOURNAL	1..49 /organism="unidentified" /db_xref="taxon:32644"					
FEATURES						
source	17 a 8 c 3 g 21 t					
BASE COUNT						
ORIGIN						
Query Match	0.9%;	Score 21.6;	DB 6;	Length 49;		
Best Local Similarity	68.2%;	Pred. No. 2e+06;				
Matches	30;	Conservative	0;	Mismatches	14;	Indels
						Gaps
						0;
Qy	2060 ATGTGCAAAATCTGTTATAGCTTTAAATATATCTGCAATTTT	2103				
Dd	2 ATTGCTTAACCTATTATATAGCATAGAATAATATTTTTCACATT	45				
RESULT 22						
	ARI24897/c					


```

SOURCE      1. .46
             /organism="synthetic construct"
             /db_xref="taxon:32630"
mRNA        complemen<1. .31)

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BASE COUNT      17 a      11 c      3 g      12 t
ORIGIN          /organism="Candida albicans
                /db_xref="taxon:5476"
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Query Match 0.9%; Score 20.8; DB 6; Length 43;
Best Local Similarity 70.0%; Pred. No. 3.1e+06;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 2047 CTGTTTGCTTTATGTCGCAAAATCTGTATAGCTTTAA 2086
Db 42 CTTTCTGGGATTTTGTGAAAGTCTGTATAGTATAGAA 3

RESULT 31
A46759/c A46759 49 bp DNA linear PAT 07-MAR-1997
LOCUS Sequence 1 from Patent EP0681027.
DEFINITION A46759
ACCESSION A46759.1 GI:2300854
VERSION
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 49)
AUTHORS Frasconi, G. and Grandi, G.
TITLE Plasmid vector and its use for the production of heterologous proteins
JOURNAL Patent: EP 0681027-A 1 08-NOV-1995;
COMMENT ENRICHES SPA (IT)
FEATURES Other publication JP 7289271 951107.
Location/Qualifiers

1..49
/organism="unidentified"
/db_xref="taxon:32644"

BASE COUNT 18 a 3 c 6 g 22 t
ORIGIN

Query Match 0.9%; Score 20.8; DB 6; Length 49;
Best Local Similarity 64.6%; Pred. No. 3.1e+06;
Matches 31; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

OY 2068 AATCTGTTAGCTTTAAATATATCTGGAACCTTTTATGATTATCCA 2115
Db 49 AATCTATATATCATTAATAAATTTCTCGAAGCAATTAATTTTCTA 2

RESULT 32
I89340/c I89340 49 bp DNA linear PAT 10-AUG-1998
LOCUS Sequence 1 from patent US 5721137.
DEFINITION I89340
ACCESSION I89340.1 GI:3409280
VERSION
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 49)
AUTHORS Frasconi, G. and Grandi, G.
TITLE Plasmid vector and its use for the production of heterologous proteins
JOURNAL Patent: US 5721137-A 1 24-FEB-1998;
FEATURES Location/Qualifiers

1..49
/organism="unknown"
/organism="unknown"

BASE COUNT 18 a 3 c 6 g 22 t
ORIGIN

Query Match 0.9%; Score 20.8; DB 6; Length 49;
Best Local Similarity 64.6%; Pred. No. 3.1e+06;
Matches 31; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

OY 2068 AATCTGTTAGCTTTAAATATATCTGGAACCTTTTATGATTATCCA 2115
Db 49 AATCTATATATCATTAATAAATTTCTCGAAGCAATTAATTTTCTA 2

RESULT 33
AXI65053/c AXI65053 50 bp DNA linear PAT 22-JUN-2001
LOCUS Sequence 248 from patent WO0138586.
DEFINITION AXI65053
ACCESSION AXI65053.1 GI:14545882
VERSION
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 50)
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0138586-A 248 31-MAY-2001;
FEATURES Curagen Corporation (US)
Location/Qualifiers

1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"

misc_feature 25..26
/note="Nucleotide deleted between bases 25 and 26"
Accession number c943992566
variation 26
/note="single nucleotide polymorphism"

BASE COUNT 26 a 5 c 7 g 12 t
ORIGIN

Query Match 0.9%; Score 20.8; DB 6; Length 50;
Best Local Similarity 70.0%; Pred. No. 3.1e+06;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 2220 AATCTGATAAATGACGCTTTTCTGCGCAATAGTAA 2259
Db 43 AATCTTGTAATGCTCTTTTCTGCTCAGATTGA 4

RESULT 34
ARI39408/c ARI39408 41 bp DNA linear PAT 16-JUN-2001
LOCUS Sequence 21 from patent US 6207373.
DEFINITION ARI39408
ACCESSION ARI39408
VERSION ARI39408.1 GI:14481904
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 41)
AUTHORS Sosnowski, R.G. and Tu, E.
TITLE Methods for determining nature of repeat units in DNA
JOURNAL Patent: US 6207373-A 21 27-MAR-2001;
FEATURES Location/Qualifiers

1..41
/organism="unknown"

BASE COUNT 16 a 5 c 10 g 10 t
ORIGIN

Query Match 0.9%; Score 20.6; DB 6; Length 41;
Best Local Similarity 74.3%; Pred. No. 3.4e+06;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1985 ATTATCCATTCATCATTTATTCATTCGCTGTC 2019
Db 40 ATTATTCATTCATTCATTCATTCATTCAGTGGGTTTC 6

RESULT 35
ARI39392/c ARI39392 45 bp DNA linear PAT 16-JUN-2001
LOCUS Sequence 5 from patent US 6207373.
DEFINITION ARI39392
ACCESSION ARI39392.1 GI:14481888
VERSION

REFERENCE 2 (bases 1 to 46)
AUTHORS Qu, L.H.
TITLE Direct Submission
JOURNAL Submitted (01-JUN-1999) Qu L.H., Biotechnology Research Center,
Zhong Shan University, Biotechnology Research Center, Zhong Shan
University, Guangzhou, CHINA
LOCATION/Qualifiers
source 1. .46
/organism="Mus musculus"
/db_xref="taxon:10090"
gene 1. .46
/gene="Z32"
snRNA 1. .>46
/gene="Z32"
/product="Z32 snRNA"
/function="methylation guide for U2 snRNA at Am30"
/evidence=experimental
BASE COUNT 15 a 4 c 11 g 16 t
ORIGIN
Query Match 0.9%; Score 20.2; DB 10; Length 46;
Best Local Similarity 68.3%; Pred. No. 4.4e+06;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
OY 2155 TAAGTGAGGAAGATTATGCAAGATTTTGGCACTTTG 2195
Db 4 TCAATGATGAAAGTTTACTACTGATTTTGCACCTGTG 44
RESULT 40
LOCUS AX161234 50 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 4562 from Patent WO0140521.
ACCESSION AX161234
VERSION AX161234.1 GI:14542565
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 4562 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
1. .50
/organism="Homo sapiens"
/db_xref="taxon:9606"
misc_feature 25. .26
/note="Nucleotide deleted between bases 25 and 26
Accession number cg43958770"
misc_feature 26
/note="2 of 2 allelic variants (4561 is other entry)"
BASE COUNT 18 a 13 c 5 g 14 t
ORIGIN
Query Match 0.9%; Score 20.2; DB 6; Length 50;
Best Local Similarity 68.3%; Pred. No. 4.4e+06;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
OY 2230 AATGACTGTTTTTTCGCTAATAGTAACTGTTAAAA 2270
Db 42 AGAAGACTCTTTTGGCCATTTTGAATCGTATAAAAA 2
RESULT 41
LOCUS AX162672 50 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6000 from Patent WO0140521.
ACCESSION AX162672
VERSION AX162672.1 GI:14544003

KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 6000 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
1. .50
/organism="Homo sapiens"
/db_xref="taxon:9606"
misc_feature 25. .26
/note="Nucleotide deleted between bases 25 and 26
Accession number cg44131756"
misc_feature 26
/note="2 of 2 allelic variants (6001 is other entry)"
BASE COUNT 25 a 4 c 17 g 4 t
ORIGIN
Query Match 0.9%; Score 20.2; DB 6; Length 50;
Best Local Similarity 68.3%; Pred. No. 4.4e+06;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
OY 1093 CTTTCGTGCTGCTTTGTTCTCTGAATTTTCAGAGACT 1133
Db 42 CTTTCGTGCTGCTTTCTTTCTTTCTTTTGTGATAGAT 2
RESULT 42
LOCUS AX162674 50 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 6002 from Patent WO0140521.
ACCESSION AX162674
VERSION AX162674.1 GI:14544005
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 6002 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
1. .50
/organism="Homo sapiens"
/db_xref="taxon:9606"
misc_feature 25. .26
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Accession number cg44131756"
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Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
OY 1093 CTTTCGTGCTGCTTTGTTCTCTGAATTTTCAGAGACT 1133
Db 41 CTTTCGTGCTGCTTTCTTTCTTTCTTTTGTGATAGAT 1
RESULT 43
LOCUS E22339 50 bp DNA linear PAT 18-JUN-2001

DEFINITION DNA encoding fructosylamino acid oxidase.
E22339
ACCESSION E22339.1 GI:13024007
KEYWORDS JP 1999046769-A/32.
SOURCE unclassified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 50)
AUTHORS Akio, K., Yasuyoshi, S., Yoshiki, T. and Hiroshi, F.
TITLE DNA encoding fructosylamino acid oxidase
JOURNAL Patent: JP 1999046769-A 32 23-FEB-1999;
KYOTO DAIICHI KAGAKU CO LTD
OS Unidentified
PN JP 1999046769-A/32
PD 23-FEB-1999
PF 05-AUG-1997 JP 1997210609
PR
PI AKIO KATO, YASUYOSHI SAKAI, YOSHIKI TANI, HIROSHI FUKUJE PC
C12N15/09, C12N1/19, C12N9/06, C12Q1/26//((C12N15/09, C12R1:80), PC
(C12N1/19, C12R1:72), (C12N9/06, C12R1:72), C12N15/00, (C12N15/00, PC
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CC Topology: Linear;
FH Key 1. .50
FT source Location/Qualifiers
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Best Local Similarity 68.3%; Pred. No. 4.4e+06;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 247 CAATGCATCATATATAACACAGACACTTGTGATAAGTGA 287
DB 49 CATATCACCATCATTAACACAGACACTTGTATATTGA 9
RESULT 44
E22344 50 bp DNA linear PAT 18-JUN-2001
LOCUS E22344
DEFINITION DNA encoding fructosylamino acid oxidase.
ACCESSION E22344.1 GI:13024012
KEYWORDS JP 1999046769-A/37.
VERSION JP 1999046769-A/37.
KEYWORDS unclassified.
SOURCE unclassified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 50)
AUTHORS Akio, K., Yasuyoshi, S., Yoshiki, T. and Hiroshi, F.
TITLE DNA encoding fructosylamino acid oxidase
JOURNAL Patent: JP 1999046769-A 37 23-FEB-1999;
KYOTO DAIICHI KAGAKU CO LTD
OS Unidentified
PN JP 1999046769-A/37
PD 23-FEB-1999
PF 05-AUG-1997 JP 1997210609
PR
PI AKIO KATO, YASUYOSHI SAKAI, YOSHIKI TANI, HIROSHI FUKUJE PC
C12N15/09, C12N1/19, C12N9/06, C12Q1/26//((C12N15/09, C12R1:80), PC
(C12N1/19, C12R1:72), (C12N9/06, C12R1:72), C12N15/00, (C12N15/00, PC
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CC Topology: Linear;
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Best Local Similarity 68.3%; Pred. No. 4.4e+06;
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DB 10 CATATCACCATCATTAACACAGACACTTGTATATTGA 50
RESULT 45
AR084536/c 36 bp DNA linear PAT 01-SEP-2000
LOCUS AR084536
DEFINITION Sequence 25 from patent US 5981185.
ACCESSION AR084536
VERSION AR084536.1 GI:10011307
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 36)
AUTHORS Watson, R.S., Coassin, P.J., Rampal, J.B. and Caskey, C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 25 09-NOV-1999;
FEATURES
source Location/Qualifiers
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Matches 26; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1892 GGAAGAGCAAGGACAGTGCAGCAGGAGAGAACAA 1927
DB 36 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1
RESULT 46
AX361209 38 bp DNA linear PAT 15-FEB-2002
LOCUS AX361209
DEFINITION Sequence 46 from Patent WO0208460.
ACCESSION AX361209
VERSION AX361209.1 GI:18693853
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Karlsson, F.
TITLE Methods for detection of human papillomavirus mrna
JOURNAL Patent: WO 0208460-A 46 31-JAN-2002;
Norchip A/S (NO)
FEATURES
source Location/Qualifiers
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/note="Oligonucleotide"
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Matches 23; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
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DB 6 AAGTGCATATGATGATGTCRTGAGAGAAVAMACT 37

RESULT	47
A07129/c	
LOCUS	A07129 39 bp DNA linear PAT 25-AUG-1993
DEFINITION	Nucleotide sequence 6 from patent number EP0258067.
ACCESSION	A07129
VERSION	A07129.1 GI:411336
KEYWORDS	.
SOURCE	unidentified.
ORGANISM	unidentified unclassified
REFERENCE	1 (bases 1 to 39)
AUTHORS	Kingsman,S.M., Wilson,M.J., Cousens,D.J. and Hinchliffe,E.
TITLE	Yeast promoter
JOURNAL	Patent: EP 0258067-A 6 02-MAR-1988; Delta Biotechnology Limited
FEATURES	Location/Qualifiers
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 Db 37 AAGATCTTTGGACATGTTTATATTTGTTGTA 2

RESULT	48
E03833/c	
LOCUS	E03833 46 bp DNA linear PAT 29-SEP-1997
DEFINITION	DNA encoding probe for gaining human thrombomodulin gene.
ACCESSION	E03833
VERSION	E03833.1 GI:2172047
KEYWORDS	JP 1992210700-A/1.
SOURCE	synthetic construct.
ORGANISM	synthetic construct.
REFERENCE	artificial sequences. 1 (bases 1 to 46)
AUTHORS	Sekano,K., Fujiwara,H., Sugiyama,N., Nawa,K. and Marumoto,Y.
TITLE	RECOMBINANT HUMAN THROMBOMODULIN DERIVATIVE
JOURNAL	Patent: JP 1992210700-A 1 31-JUL-1992;
COMMENT	DAI ICHI SEIYAKU CO LTD OS Artificial gene

PF	12-DEC-1990 JP 1990409855
PI	SAKANO KATSUTACHI, FUJIWARA HIROYUKI, SUGIYAMA NORIHUMI, PI
PI	NAMA KATSUHIKO,
PI	MARUMOTO YASUMASA
PC	C07K13/00,A61K37/02,C12N5/10,C12N15/12,C12N15/85,C12P21/02, PC
	(C12N5/10
PC	C12N1:91),(C12N15/85,C12R1:91),(C12P21/02,C12R1:91); CC
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CC	hypothetical: No;
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FT	/note='DNA probe for gaining human FT

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Db 44 TGGGGGTGAGGAGGCACAGGCTTCTGACGAGGCCAGGCTCCTG 1

RESULT	49				
LOCUS	AR059781/c				
DEFINITION	Sequence 31 from patent US 5840520.	50 bp	DNA		
ACCESSION	AR059781				linear
VERSION	AR059781.1	GI:5986231			PAT 29-SEP-1999
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				

REFERENCE	1 (bases 1 to 50)
AUTHORS	Clarke,D,Kirkwood, and Palase,P.M.
TITLE	Recombinant negative strand RNA virus expression systems
JOURNAL	Patent: US 5840520-A 31 24-NOV-1998;
FEATURES	Location/Qualifiers

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QY 2083 TAAATATATCTGGAACCTTTTAGATTATTTCCAAGCCTATTTT 2126
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 Db 48 TTAATTTAAGTGTACTTATCAAAATTCCTATTTTGCCCATTTT 5

RESULT	50			
LOCUS	E60006	45 bp	DNA	linear
DEFINITION	Ceramide-binding peptide.			
ACCESSION	E60006			
VERSION	E60006.1	GI:18622765		
KEYWORDS	JP 2000319296-A/6.			
SOURCE	synthetic construct.			
ORGANISM	synthetic construct			

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 45)	Ishikawa, M., Tanaka, Y., Ogino, K. and Taki, T.	Ceramide-binding peptide	Patent: JP 2000319296-A 6 21-NOV-2000;	
	OTSUKA PHARMACEUT CO LTD	OS	Artificial Sequence	

```
PI MASARU ISHIKAWA, YOSHINORI TANAKA, KOICHI OGINO, TAKAO TAKI PC
C07K7/00
CC
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FT source 1..45
FT /organism='Artificial Sequence'.
FT Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT      5 a      7 c      14 g      19 t
ORIGIN

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Searched: 441362 seqs, 15338381 residues

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Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	28	1.2	28	2	US-08-859-998-1322	Sequence 1322, Ap
C 2	28	1.2	28	4	US-09-225-928-1322	Sequence 1322, Ap
C 3	27.4	1.2	29	4	US-09-382-155-37	Sequence 37, Appl
C 4	27.4	1.2	29	4	US-09-382-155-38	Sequence 38, Appl
C 5	27	1.2	27	2	US-08-859-998-1226	Sequence 1226, Ap
C 6	27	1.2	27	2	US-09-225-928-1226	Sequence 1226, Ap
C 7	26	1.1	26	2	US-08-859-998-1225	Sequence 1225, Ap
C 8	26	1.1	26	2	US-08-859-998-1321	Sequence 1321, Ap
C 9	26	1.1	26	4	US-09-225-928-1225	Sequence 1225, Ap
C 10	26	1.1	26	4	US-09-225-928-1321	Sequence 1321, Ap
C 11	22.8	1.0	41	4	US-09-171-162B-11	Sequence 11, Appl
C 12	22.8	1.0	49	4	US-09-030-156-6	Sequence 6, Appl
C 13	22.8	1.0	49	4	US-09-645-757-6	Sequence 6, Appl
C 14	21.8	0.9	37	4	US-09-171-162B-12	Sequence 12, Appl
C 15	21.8	0.9	38	4	US-09-545-481-7	Sequence 7, Appl
C 16	21.8	0.9	49	4	US-09-710-200-59	Sequence 59, Appl
C 17	21.4	0.9	45	4	US-09-109-207C-27	Sequence 27, Appl
C 18	21.4	0.9	48	4	US-09-305-408-9	Sequence 9, Appl
C 19	21.2	0.9	48	4	US-09-358-972-150	Sequence 150, Appl
C 20	21.2	0.9	48	4	US-09-383-316-44	Sequence 44, Appl
C 21	21	0.9	21	4	US-08-556-627A-7	Sequence 7, Appl
C 22	20.8	0.9	41	4	US-09-564-805-130	Sequence 130, Appl
C 23	20.8	0.9	49	1	US-08-400-864-1	Sequence 1, Appl
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C 25	20.6	0.9	41	4	US-09-645-757-21	Sequence 21, Appl
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C 27	20.6	0.9	45	4	US-09-645-757-5	Sequence 5, Appl

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C 30	20	0.9	36	2	US-08-863-639A-25	Sequence 25, Appl
C 31	20	0.9	42	3	US-08-938-830-31	Sequence 31, Appl
C 32	20	0.9	47	4	US-09-641-638-1118	Sequence 1118, Ap
C 33	20	0.9	50	2	US-08-316-439A-31	Sequence 31, Appl
C 34	19.8	0.9	43	4	US-09-276-533A-6	Sequence 6, Appl
C 35	19.8	0.9	47	4	US-09-158-863C-32	Sequence 32, Appl
C 36	19.6	0.8	31	4	US-09-171-162B-13	Sequence 13, Appl
C 37	19.6	0.8	42	5	PCT-US96-03916-35	Sequence 35, Appl
C 38	19.6	0.8	49	2	US-08-801-898A-27	Sequence 27, Appl
C 39	19.4	0.8	21	4	US-08-556-627A-9	Sequence 9, Appl
C 40	19.4	0.8	40	1	US-08-231-342-17	Sequence 17, Appl
C 41	19.4	0.8	47	4	US-09-345-882-71	Sequence 71, Appl
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C 43	19.2	0.8	41	2	US-08-484-397A-17	Sequence 17, Appl
C 44	19.2	0.8	41	4	US-09-546-483-2	Sequence 2, Appl
C 45	19.2	0.8	41	4	US-09-823-177-2	Sequence 2, Appl
C 46	19.2	0.8	42	3	US-08-746-111-40	Sequence 40, Appl
C 47	19.2	0.8	45	4	US-09-284-832-29	Sequence 29, Appl
C 48	19.2	0.8	47	4	US-09-641-638-931	Sequence 931, Appl
C 49	19.2	0.8	48	1	US-08-471-791-35	Sequence 35, Appl
C 50	19.2	0.8	48	5	PCT-US91-01746-35	Sequence 35, Appl
C 51	19.2	0.8	50	4	US-09-315-886C-13	Sequence 13, Appl
C 52	19.2	0.8	50	4	US-08-973-005A-2	Sequence 2, Appl
C 53	19	0.8	19	4	US-08-556-627A-5	Sequence 5, Appl
C 54	19	0.8	41	3	US-08-813-507-35	Sequence 35, Appl
C 55	19	0.8	41	4	US-09-464-453-35	Sequence 35, Appl
C 56	19	0.8	45	3	US-08-213-741-6	Sequence 6, Appl
C 57	19	0.8	45	4	US-08-522-336-6	Sequence 6, Appl
C 58	19	0.8	46	4	US-09-537-357-8	Sequence 8, Appl
C 59	19	0.8	48	3	US-08-933-358-20	Sequence 20, Appl
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C 72	18.8	0.8	48	1	US-08-171-389-226	Sequence 226, Appl
C 73	18.8	0.8	48	1	US-08-123-936-226	Sequence 226, Appl
C 74	18.8	0.8	48	2	US-08-475-228A-226	Sequence 226, Appl
C 75	18.8	0.8	48	3	US-08-482-080A-226	Sequence 226, Appl
C 76	18.8	0.8	48	4	US-09-354-947-226	Sequence 226, Appl
C 77	18.8	0.8	48	5	PCT-US93-12388-226	Sequence 226, Appl
C 78	18.8	0.8	50	2	US-08-190-199A-4	Sequence 4, Appl
C 79	18.8	0.8	50	2	US-08-316-439A-37	Sequence 37, Appl
C 80	18.6	0.8	34	3	US-08-793-666-3	Sequence 3, Appl
C 81	18.6	0.8	39	4	US-09-535-755-13	Sequence 13, Appl
C 82	18.6	0.8	40	1	US-07-854-596B-13	Sequence 13, Appl
C 83	18.6	0.8	40	2	US-09-076-193-1	Sequence 1, Appl
C 84	18.6	0.8	40	4	US-09-307-925-1	Sequence 1, Appl
C 85	18.6	0.8	41	4	US-09-030-156-4	Sequence 4, Appl
C 86	18.6	0.8	41	4	US-09-645-757-4	Sequence 4, Appl
C 87	18.6	0.8	42	1	US-08-253-877C-50	Sequence 50, Appl
C 88	18.6	0.8	42	2	US-08-452-164A-50	Sequence 50, Appl
C 89	18.6	0.8	50	1	US-08-171-389-467	Sequence 467, Appl
C 90	18.6	0.8	50	1	US-08-171-389-469	Sequence 467, Appl
C 91	18.6	0.8	50	1	US-08-123-936-467	Sequence 467, Appl
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C 94	18.6	0.8	50	2	US-08-475-228A-469	Sequence 469, Appl
C 95	18.6	0.8	50	2	US-08-053-451B-95	Sequence 95, Appl
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C 99	18.6	0.8	50	4	US-09-354-947-469	Sequence 469, Appl
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C 248	17.6	0.8	50	4	US-09-399-773-23	Sequence 23, Appl	321	17.2	0.7	49	2	US-08-756-506-18	Sequence 18, Appl
C 249	17.6	0.8	50	4	US-09-354-947-471	Sequence 471, App	322	17.2	0.7	49	2	PCT-US95-05602-21	Sequence 21, Appl
C 250	17.6	0.8	50	5	PCT-US93-12388-471	Sequence 471, App	323	17.2	0.7	49	5	PCT-US95-05816-21	Sequence 21, Appl
C 251	17.4	0.8	30	2	US-08-331-081B-14	Sequence 14, Appl	324	17.2	0.7	50	1	US-07-718-490-1	Sequence 1, Appl
C 252	17.4	0.8	30	3	US-08-738-381-23	Sequence 23, Appl	325	17.2	0.7	50	1	US-08-171-389-344	Sequence 344, App
C 253	17.4	0.8	36	1	US-07-841-662-16	Sequence 16, Appl	326	17.2	0.7	50	1	US-08-171-389-390	Sequence 390, App
C 254	17.4	0.8	36	1	US-08-209-797-16	Sequence 16, Appl	327	17.2	0.7	50	1	US-08-207-901-55	Sequence 55, Appl
C 255	17.4	0.8	36	1	US-08-669-685-16	Sequence 16, Appl	328	17.2	0.7	50	1	US-08-123-936-344	Sequence 344, App
C 256	17.4	0.8	36	3	US-09-103-486-16	Sequence 16, Appl	329	17.2	0.7	50	1	US-08-123-936-390	Sequence 390, App
C 257	17.4	0.8	36	4	US-09-039-982A-16	Sequence 16, Appl	330	17.2	0.7	50	1	US-08-475-228A-344	Sequence 344, App
C 258	17.4	0.8	36	4	US-09-039-641-16	Sequence 16, Appl	331	17.2	0.7	50	2	US-08-475-228A-390	Sequence 390, App
C 259	17.4	0.8	36	4	US-09-039-762A-16	Sequence 16, Appl	332	17.2	0.7	50	3	US-08-482-080A-344	Sequence 344, App
C 260	17.4	0.8	36	4	US-09-042-492D-16	Sequence 16, Appl	333	17.2	0.7	50	3	US-08-482-080A-390	Sequence 390, App
C 261	17.4	0.8	36	5	PCT-US93-01557-16	Sequence 16, Appl	334	17.2	0.7	50	4	US-09-354-947-344	Sequence 344, App
C 262	17.4	0.8	36	5	PCT-US93-01557-16	Sequence 16, Appl	335	17.2	0.7	50	4	US-09-354-947-390	Sequence 390, App
C 263	17.4	0.8	40	4	US-09-086-726-10	Sequence 10, Appl	336	17.2	0.7	50	5	PCT-US93-12388-344	Sequence 344, App
C 264	17.4	0.8	41	4	US-09-191-468-12	Sequence 12, Appl	337	17.2	0.7	50	5	PCT-US93-12388-390	Sequence 390, App
C 265	17.4	0.8	42	2	US-08-452-724A-43	Sequence 43, Appl	338	17.2	0.7	27	3	US-09-192-048-8	Sequence 8, Appl
C 266	17.4	0.8	43	4	US-09-387-300-36	Sequence 36, Appl	339	17.2	0.7	27	3	US-08-874-460-7	Sequence 7, Appl
C 267	17.4	0.8	44	1	US-08-086-634-8	Sequence 8, Appl	340	17.2	0.7	30	2	US-08-874-460-7	Sequence 7, Appl
C 268	17.4	0.8	44	2	US-08-350-260A-558	Sequence 558, App	341	17.2	0.7	30	3	US-09-130-663-9	Sequence 9, Appl
C 269	17.4	0.8	44	4	US-09-358-036-24	Sequence 24, Appl	342	17.2	0.7	30	3	US-09-614-022-9	Sequence 9, Appl
C 270	17.4	0.8	44	4	US-09-097-239-24	Sequence 24, Appl	343	17.2	0.7	32	4	US-08-616-853-17	Sequence 17, Appl
C 271	17.4	0.8	44	4	US-09-301-593-73	Sequence 73, Appl	344	17.2	0.7	32	1	US-08-616-853-17	Sequence 17, Appl
C 272	17.4	0.8	47	2	US-08-467-603-98	Sequence 98, Appl	345	17.2	0.7	32	3	US-08-850-049-89	Sequence 89, Appl
C 273	17.4	0.8	47	2	US-08-811-897A-51	Sequence 51, Appl	346	17.2	0.7	33	2	US-08-050-478-89	Sequence 89, Appl
C 274	17.4	0.8	47	2	US-08-166-793-98	Sequence 98, Appl	347	17.2	0.7	33	4	US-09-414-117-89	Sequence 89, Appl
C 275	17.4	0.8	47	2	US-08-855-213-51	Sequence 51, Appl	348	17.2	0.7	33	4	US-09-678-437-89	Sequence 89, Appl
C 276	17.4	0.8	47	2	US-08-491-861A-98	Sequence 98, Appl	349	17.2	0.7	33	4	US-08-428-733A-22	Sequence 22, Appl
C 277	17.4	0.8	47	4	US-09-201-474-51	Sequence 51, Appl	350	17.2	0.7	34	1	US-08-428-733A-25	Sequence 25, Appl
C 278	17.4	0.8	47	4	US-09-641-638-1081	Sequence 1081, App	351	17.2	0.7	34	1	US-08-544-381B-174	Sequence 174, App
C 279	17.4	0.8	47	4	US-09-641-638-1202	Sequence 1202, App	352	17.2	0.7	34	3	US-08-732-708C-45	Sequence 45, Appl
C 280	17.4	0.8	50	3	US-08-985-162-1671	Sequence 1671, App	353	17.2	0.7	34	3	US-08-732-708C-45	Sequence 45, Appl
C 281	17.4	0.8	50	4	US-08-991-789A-269	Sequence 269, App	354	17.2	0.7	35	4	US-09-101-629A-34	Sequence 34, Appl
C 282	17.4	0.8	50	4	US-09-062-451-269	Sequence 269, App	355	17.2	0.7	35	1	US-08-364-339-10	Sequence 10, Appl
C 283	17.2	0.7	27	2	US-08-670-186-9	Sequence 9, Appl	356	17.2	0.7	35	1	US-08-487-034-16	Sequence 16, Appl
C 284	17.2	0.7	31	3	US-08-848-373-1	Sequence 1, Appl	357	17.2	0.7	35	3	US-08-577-121-23	Sequence 23, Appl
C 285	17.2	0.7	31	3	US-08-670-186-9	Sequence 9, Appl	358	17.2	0.7	35	4	US-08-985-700-23	Sequence 23, Appl
C 286	17.2	0.7	31	5	PCT-US92-10792-29	Sequence 29, Appl	359	17.2	0.7	35	5	PCT-US95-16916-23	Sequence 23, Appl
C 287	17.2	0.7	33	4	US-09-023-082A-144	Sequence 144, App	360	17.2	0.7	36	2	US-08-596-387B-114	Sequence 114, App
C 288	17.2	0.7	34	4	US-09-043-646-6	Sequence 6, Appl	361	17.2	0.7	36	2	US-08-374-483-9	Sequence 9, Appl
C 289	17.2	0.7	35	4	US-09-266-464-4	Sequence 4, Appl	362	17.2	0.7	36	4	US-09-067-615-114	Sequence 114, App
C 290	17.2	0.7	36	2	US-08-174-672D-34	Sequence 34, Appl	363	17.2	0.7	36	5	PCT-US95-09883A-114	Sequence 114, App
C 291	17.2	0.7	37	4	US-08-361-337-43	Sequence 43, Appl	364	17.2	0.7	36	5	US-08-105-483-402	Sequence 402, App
C 292	17.2	0.7	37	4	US-09-472-146A-1	Sequence 1, Appl	365	17.2	0.7	38	1	US-08-709-209-402	Sequence 402, App
C 293	17.2	0.7	38	4	US-08-686-968C-98	Sequence 98, Appl	366	17.2	0.7	38	1	US-08-303-275-106	Sequence 106, App
C 294	17.2	0.7	39	1	US-08-706-037-9	Sequence 9, Appl	367	17.2	0.7	38	1	US-08-458-101-402	Sequence 402, App
C 295	17.2	0.7	39	1	US-08-636-876-14	Sequence 14, Appl	368	17.2	0.7	39	4	US-08-946-475-12	Sequence 12, Appl
C 296	17.2	0.7	39	2	US-09-005-397-9	Sequence 9, Appl	369	17.2	0.7	39	3	US-08-946-475-12	Sequence 12, Appl
C 297	17.2	0.7	39	6	5520913-17	Patent No. 5520913	370	17.2	0.7	39	4	US-09-052-993-3	Sequence 3, Appl
C 298	17.2	0.7	40	1	US-08-436-463-12	Sequence 12, Appl	371	17.2	0.7	39	4	US-08-340-479-12	Sequence 12, Appl
C 299	17.2	0.7	40	2	US-08-665-040-9	Sequence 9, Appl	372	17.2	0.7	40	4	US-08-481-659C-22	Sequence 22, Appl
C 300	17.2	0.7	40	4	US-08-189-462-25	Sequence 25, Appl	373	17.2	0.7	41	4	US-09-233-086-25	Sequence 25, Appl
C 301	17.2	0.7	40	4	US-09-189-462-26	Sequence 26, Appl	374	17.2	0.7	41	4	US-07-723-002C-18	Sequence 18, Appl
C 302	17.2	0.7	41	1	US-08-333-894-1	Sequence 1, Appl	375	17.2	0.7	42	1	US-08-464-136-75	Sequence 75, Appl
C 303	17.2	0.7	42	1	US-08-391-000-36	Sequence 36, Appl	376	17.2	0.7	42	2	US-08-349-131-75	Sequence 75, Appl
C 304	17.2	0.7	42	2	US-08-741-931-36	Sequence 36, Appl	377	17.2	0.7	42	2	US-08-975-902-10	Sequence 10, Appl
C 305	17.2	0.7	42	2	US-08-612-858-37	Sequence 37, Appl	378	17.2	0.7	42	2	US-08-053-451B-91	Sequence 91, Appl
C 306	17.2	0.7	43	2	US-08-756-506-19	Sequence 19, Appl	379	17.2	0.7	42	3	US-08-470-297A-75	Sequence 75, Appl
C 307	17.2	0.7	43	2	US-08-676-279-11	Sequence 11, Appl	380	17.2	0.7	42	3	US-09-251-565-10	Sequence 10, Appl
C 308	17.2	0.7	43	2	US-08-452-242-21	Sequence 21, Appl	381	17.2	0.7	42	3	US-09-193-191-12	Sequence 12, Appl
C 309	17.2	0.7	46	3	US-08-453-176A-21	Sequence 21, Appl	382	17.2	0.7	42	4	US-09-138-277C-6	Sequence 6, Appl
C 310	17.2	0.7	46	3	US-08-451-374-21	Sequence 21, Appl	383	17.2	0.7	42	5	US-09-359-304B-23	Sequence 23, Appl
C 311	17.2	0.7	46	4	US-08-935-268A-21	Sequence 21, Appl	384	17.2	0.7	42	5	PCT-US91-07149-75	Sequence 75, Appl
C 312	17.2	0.7	46	4	US-08-452-229-21	Sequence 21, Appl	385	17.2	0.7	43	1	US-07-885-688A-4	Sequence 4, Appl
C 313	17.2	0.7	47	4	US-09-360-237-52	Sequence 52, Appl	386	17.2	0.7	44	3	US-08-726-807B-28	Sequence 28, Appl
C 314	17.2	0.7	47	4	US-09-641-638-1248	Sequence 1248, App	387	17.2	0.7	44	3	US-08-726-807B-41	Sequence 41, Appl
C 315	17.2	0.7	48	1	US-08-319-836B-15	Sequence 15, Appl	388	17.2	0.7	44	3	US-09-258-367-28	Sequence 28, Appl
C 316	17.2	0.7	48	5	PCT-US95-13142-15	Sequence 15, Appl	389	17.2	0.7	44	3	US-09-258-367-41	Sequence 41, Appl
C 317	17.2	0.7	49	1	US-08-115-497-5	Sequence 5, Appl	390	17.2	0.7	44	4	US-09-546-550-28	Sequence 28, Appl
C 318	17.2	0.7	49	1	US-08-242-403A-21	Sequence 21, Appl	391	17.2	0.7	44	4	US-09-546-550-41	Sequence 41, Appl
C 319	17.2	0.7	49	1	US-08-774-128-21	Sequence 21, Appl	392	17.2	0.7	44	4	US-09-431-414-28	Sequence 28, Appl

C 393	17	0.7	44	4	US-09-431-414-41	Sequence 41, Appl	C 466	16.8	0.7	36	1	US-08-197-791-23	Sequence 23, Appl
C 394	17	0.7	44	4	US-09-225-670-28	Sequence 28, Appl	C 467	16.8	0.7	36	1	US-08-411-795B-410	Sequence 410, App
C 395	17	0.7	44	4	US-09-225-670-41	Sequence 41, Appl	C 468	16.8	0.7	36	1	US-08-469-319A-410	Sequence 410, App
C 396	17	0.7	44	4	US-09-431-349C-28	Sequence 28, Appl	C 469	16.8	0.7	36	2	US-08-124-981A-7	Sequence 7, Appl
C 397	17	0.7	44	4	US-09-431-349C-41	Sequence 41, Appl	C 470	16.8	0.7	36	3	US-09-037-192-5	Sequence 5, Appl
C 398	17	0.7	45	1	US-08-145-681-9	Sequence 9, Appl	C 471	16.8	0.7	36	3	US-09-037-192-5	Sequence 5, Appl
C 399	17	0.7	45	1	US-08-483-415-24	Sequence 24, Appl	C 472	16.8	0.7	36	3	US-08-833-167-12	Sequence 12, Appl
C 400	17	0.7	45	1	US-08-453-703-9	Sequence 9, Appl	C 473	16.8	0.7	36	3	US-09-037-143-5	Sequence 5, Appl
C 401	17	0.7	45	2	US-08-456-106-9	Sequence 9, Appl	C 474	16.8	0.7	36	3	US-09-049-691-5	Sequence 5, Appl
C 402	17	0.7	45	3	US-08-961-083-235	Sequence 235, App	C 475	16.8	0.7	36	4	US-08-260-174-5	Sequence 5, Appl
C 403	17	0.7	45	4	US-09-265-577-9	Sequence 9, Appl	C 476	16.8	0.7	36	4	US-09-338-128A-5	Sequence 5, Appl
C 404	17	0.7	45	4	US-09-627-216A-3	Sequence 3, Appl	C 477	16.8	0.7	36	4	US-09-232-343-5	Sequence 5, Appl
C 405	17	0.7	45	6	5487983-21	Patent No. 5487983	C 478	16.8	0.7	36	4	US-09-344-837A-12	Sequence 5, Appl
C 406	17	0.7	46	1	US-08-171-389-287	Sequence 287, App	C 479	16.8	0.7	36	4	US-09-383-143-44	Sequence 44, Appl
C 407	17	0.7	46	1	US-08-123-936-287	Sequence 287, App	C 480	16.8	0.7	36	4	US-09-037-192-5	Sequence 5, Appl
C 408	17	0.7	46	2	US-08-475-228A-287	Sequence 287, App	C 481	16.8	0.7	36	4	US-08-764-111A-410	Sequence 410, App
C 409	17	0.7	46	2	US-08-482-080A-287	Sequence 287, App	C 482	16.8	0.7	36	4	US-08-469-419-410	Sequence 410, App
C 410	17	0.7	46	3	US-08-961-810-93	Sequence 93, Appl	C 483	16.8	0.7	37	4	US-09-030-156-3	Sequence 3, Appl
C 411	17	0.7	46	4	US-08-352-902D-93	Sequence 287, App	C 484	16.8	0.7	37	4	US-09-645-757-3	Sequence 3, Appl
C 412	17	0.7	46	4	US-09-641-638-892	Sequence 892, App	C 485	16.8	0.7	38	1	US-08-373-128A-2118	Sequence 2118, Ap
C 413	17	0.7	46	4	US-09-641-638-1207	Sequence 1207, Ap	C 486	16.8	0.7	38	1	US-08-435-628-2118	Sequence 2118, Ap
C 414	17	0.7	46	4	US-07-854-603-21	Sequence 21, Appl	C 487	16.8	0.7	38	4	US-09-031-563-10	Sequence 10, Appl
C 415	17	0.7	46	5	US-08-105-483-102	Sequence 102, App	C 488	16.8	0.7	39	1	US-09-392-277-10	Sequence 10, Appl
C 416	17	0.7	47	2	US-08-936-387-8	Sequence 287, App	C 489	16.8	0.7	39	3	US-08-801-154-11	Sequence 18, Appl
C 417	17	0.7	47	4	US-09-641-638-892	Sequence 892, App	C 490	16.8	0.7	39	4	US-09-437-038B-19	Sequence 19, Appl
C 418	17	0.7	47	4	US-09-641-638-1207	Sequence 1207, Ap	C 491	16.8	0.7	39	4	US-09-316-083-30	Sequence 30, Appl
C 419	17	0.7	48	1	US-07-854-603-21	Sequence 21, Appl	C 492	16.8	0.7	39	4	US-09-316-083-30	Sequence 30, Appl
C 420	17	0.7	48	1	US-07-854-603-21	Sequence 21, Appl	C 493	16.8	0.7	39	4	US-09-316-083-30	Sequence 30, Appl
C 421	17	0.7	48	1	US-07-854-603-21	Sequence 21, Appl	C 494	16.8	0.7	39	4	US-09-316-083-30	Sequence 30, Appl
C 422	17	0.7	49	1	US-08-105-483-102	Sequence 102, App	C 495	16.8	0.7	40	3	US-08-874-825-9	Sequence 9, Appl
C 423	17	0.7	49	1	US-08-105-483-103	Sequence 103, App	C 496	16.8	0.7	40	3	US-08-874-825-25	Sequence 25, Appl
C 424	17	0.7	49	1	US-08-207-901-60	Sequence 60, Appl	C 497	16.8	0.7	40	3	US-08-663-824-9	Sequence 9, Appl
C 425	17	0.7	49	1	US-08-709-209-102	Sequence 102, App	C 498	16.8	0.7	40	3	US-08-663-824-25	Sequence 25, Appl
C 426	17	0.7	49	1	US-08-709-209-103	Sequence 103, App	C 499	16.8	0.7	40	3	US-08-663-824-25	Sequence 25, Appl
C 427	17	0.7	49	1	US-08-257-073-112	Sequence 112, App	C 500	16.8	0.7	40	4	US-09-231-303-9	Sequence 9, Appl
C 428	17	0.7	49	1	US-08-458-101-103	Sequence 103, App	C 501	16.8	0.7	41	1	US-07-860-468-14	Sequence 14, Appl
C 429	17	0.7	49	2	US-08-801-898A-29	Sequence 29, Appl	C 502	16.8	0.7	41	1	US-07-860-468-15	Sequence 15, Appl
C 430	17	0.7	49	4	US-09-091-814-111	Sequence 111, App	C 503	16.8	0.7	42	1	US-07-931-473B-284	Sequence 284, App
C 431	17	0.7	49	4	US-08-171-389-383	Sequence 383, App	C 504	16.8	0.7	42	1	US-07-714-131C-284	Sequence 284, App
C 432	17	0.7	50	1	US-08-123-936-383	Sequence 383, App	C 505	16.8	0.7	42	1	US-08-412-110-284	Sequence 284, App
C 433	17	0.7	50	1	US-08-123-936-383	Sequence 383, App	C 506	16.8	0.7	42	1	US-08-409-442A-284	Sequence 284, App
C 434	17	0.7	50	1	US-08-123-936-383	Sequence 383, App	C 507	16.8	0.7	42	1	US-08-455-633A-11	Sequence 11, Appl
C 435	17	0.7	50	2	US-08-475-228A-383	Sequence 383, App	C 508	16.8	0.7	42	2	US-08-456-609A-284	Sequence 284, App
C 436	17	0.7	50	2	US-08-475-228A-383	Sequence 383, App	C 509	16.8	0.7	42	2	US-08-456-609A-284	Sequence 284, App
C 437	17	0.7	50	2	US-08-475-228A-383	Sequence 383, App	C 510	16.8	0.7	42	2	US-08-456-609A-284	Sequence 284, App
C 438	17	0.7	50	2	US-08-475-228A-383	Sequence 383, App	C 511	16.8	0.7	42	2	US-08-456-609A-284	Sequence 284, App
C 439	17	0.7	50	3	US-08-482-080A-383	Sequence 383, App	C 512	16.8	0.7	42	4	US-09-198-119C-29	Sequence 29, App
C 440	17	0.7	50	3	US-08-482-080A-383	Sequence 383, App	C 513	16.8	0.7	42	4	US-09-225-322B-13	Sequence 13, Appl
C 441	17	0.7	50	3	US-08-985-162-1688	Sequence 1688, App	C 514	16.8	0.7	42	5	PCT-US94-05354-11	Sequence 11, Appl
C 442	17	0.7	50	3	US-08-985-162-1688	Sequence 1688, App	C 515	16.8	0.7	43	1	US-08-403-762A-24	Sequence 24, Appl
C 443	17	0.7	50	4	US-09-354-947-383	Sequence 383, App	C 516	16.8	0.7	43	1	US-08-454-683-7	Sequence 7, Appl
C 444	17	0.7	50	4	US-09-354-947-383	Sequence 383, App	C 517	16.8	0.7	43	1	US-08-454-683-7	Sequence 7, Appl
C 445	17	0.7	50	4	US-09-354-947-383	Sequence 383, App	C 518	16.8	0.7	43	1	US-08-454-683-7	Sequence 7, Appl
C 446	17	0.7	50	5	PCT-US93-12388-383	Sequence 383, App	C 519	16.8	0.7	43	1	US-08-454-683-7	Sequence 7, Appl
C 447	17	0.7	50	5	PCT-US93-12388-383	Sequence 383, App	C 520	16.8	0.7	43	2	US-08-454-683-7	Sequence 7, Appl
C 448	17	0.7	50	5	PCT-US93-12388-383	Sequence 383, App	C 521	16.8	0.7	43	2	US-08-454-683-7	Sequence 7, Appl
C 449	17	0.7	50	5	PCT-US93-12388-383	Sequence 383, App	C 522	16.8	0.7	43	2	US-08-454-683-7	Sequence 7, Appl
C 450	17	0.7	50	5	PCT-US93-12388-383	Sequence 383, App	C 523	16.8	0.7	43	2	US-08-454-683-7	Sequence 7, Appl
C 451	17	0.7	50	5	PCT-US93-12388-383	Sequence 383, App	C 524	16.8	0.7	43	2	US-08-454-683-7	Sequence 7, Appl
C 452	17	0.7	50	5	PCT-US93-12388-383	Sequence 383, App	C 525	16.8	0.7	43	2	US-08-454-683-7	Sequence 7, Appl
C 453	17	0.7	50	5	PCT-US93-12388-383	Sequence 383, App	C 526	16.8	0.7	43	2	US-08-454-683-7	Sequence 7, Appl
C 454	17	0.7	50	5	PCT-US93-12388-383	Sequence 383, App	C 527	16.8	0.7	43	2	US-08-454-683-7	Sequence 7, Appl
C 455	17	0.7	50	5	PCT-US93-12388-383	Sequence 383, App	C 528	16.8	0.7	43	2	US-08-454-683-7	Sequence 7, Appl
C 456	17	0.7	50	5	PCT-US93-12388-383	Sequence 383, App	C 529	16.8	0.7	43	2	US-08-454-683-7	Sequence 7, Appl
C 457	17	0.7	50	5	PCT-US93-12388-383	Sequence 383, App	C 530	16.8	0.7	43	2	US-08-454-683-7	Sequence 7, Appl
C 458	17	0.7	50	5	PCT-US93-12388-383	Sequence 383, App	C 531	16.8	0.7	43	2	US-08-454-683-7	Sequence 7, Appl
C 459	17	0.7	50	5	PCT-US93-12388-383	Sequence 383, App	C 532	16.8	0.7	43	2	US-08-454-683-7	Sequence 7, Appl
C 460	17	0.7	50	5	PCT-US93-12388-383	Sequence 383, App	C 533	16.8	0.7	43	2	US-08-454-683-7	Sequence 7, Appl
C 461	17	0.7	50	5	PCT-US93-12388-383	Sequence 383, App	C 534	16.8	0.7	43	2	US-08-454-683-7	Sequence 7, Appl
C 462	17	0.7	50	5	PCT-US93-12388-383	Sequence 383, App	C 535	16.8	0.7	43	2	US-08-454-683-7	Sequence 7, Appl
C 463	17	0.7	50	5	PCT-US93-12388-383	Sequence 383, App	C 536	16.8	0.7	43	2	US-08-454-683-7	Sequence 7, Appl
C 464	17	0.7	50	5	PCT-US93-12388-383	Sequence 383, App	C 537	16.8	0.7	43	2	US-08-454-683-7	Sequence 7, Appl
C 465	17	0.7	50	5	PCT-US93-12388-383	Sequence 383, App	C 538	16.8	0.7	43	2	US-08-454-683-7	Sequence 7, Appl

C 539	16.8	0.7	45	4	US-08-976-183A-26	Sequence 26, Appl	612	16.6	0.7	40	4	US-09-306-998-25	Sequence 25, Appl
540	16.8	0.7	45	4	US-08-764-114-171	Sequence 171, App	C 613	16.6	0.7	40	4	US-09-225-645-11	Sequence 11, Appl
541	16.8	0.7	45	4	US-08-469-419-171	Sequence 171, App	C 614	16.6	0.7	40	4	US-09-225-645-17	Sequence 17, Appl
542	16.8	0.7	46	1	US-08-599-252-78	Sequence 78, Appl	C 615	16.6	0.7	40	4	US-08-887-534A-103	Sequence 103, App
543	16.8	0.7	46	1	US-08-436-074-51	Sequence 51, Appl	C 616	16.6	0.7	41	1	US-08-168-917-9	Sequence 9, Appl1
544	16.8	0.7	46	5	PCT-US96-06352-78	Sequence 78, Appl	C 617	16.6	0.7	41	1	US-08-244-722-3	Sequence 9, Appl1
545	16.8	0.7	46	5	PCT-US96-06583-78	Sequence 78, Appl	C 618	16.6	0.7	41	2	US-08-460-510-9	Sequence 9, Appl1
546	16.8	0.7	47	2	US-08-936-387-9	Sequence 9, Appl1	C 619	16.6	0.7	41	1	US-08-460-490-9	Sequence 9, Appl1
547	16.8	0.7	47	3	US-08-464-582-8	Sequence 8, Appl1	C 620	16.6	0.7	41	4	US-09-035-665-7	Sequence 7, Appl1
548	16.8	0.7	47	3	US-08-464-582-9	Sequence 9, Appl1	C 621	16.6	0.7	41	5	PCT-US92-00730-9	Sequence 9, Appl1
549	16.8	0.7	47	4	US-08-462-513-8	Sequence 8, Appl1	C 622	16.6	0.7	41	5	PCT-US92-10430-4	Sequence 4, Appl1
550	16.8	0.7	47	4	US-08-462-513-9	Sequence 9, Appl1	C 623	16.6	0.7	42	1	US-08-464-531-64	Sequence 64, Appl1
551	16.8	0.7	47	4	US-09-641-638-748	Sequence 748, App	C 624	16.6	0.7	42	1	US-08-487-037-8	Sequence 8, Appl1
552	16.8	0.7	47	4	US-09-641-638-759	Sequence 759, App	C 625	16.6	0.7	42	2	US-08-461-598-64	Sequence 64, Appl
553	16.8	0.7	47	4	US-09-641-638-1237	Sequence 1237, Ap	C 626	16.6	0.7	42	2	US-08-053-451B-89	Sequence 89, Appl
554	16.8	0.7	48	1	US-08-602-036A-12	Sequence 12, Appl	C 627	16.6	0.7	42	3	US-08-322-137-64	Sequence 64, Appl
555	16.8	0.7	48	1	US-08-389-459A-14	Sequence 14, Appl	C 628	16.6	0.7	42	3	US-08-322-137-20	Sequence 20, Appl
556	16.8	0.7	48	1	US-08-502-374A-12	Sequence 12, Appl	C 629	16.6	0.7	42	4	US-08-582-333A-72	Sequence 72, Appl
557	16.8	0.7	48	2	US-08-642-407A-12	Sequence 12, Appl	C 630	16.6	0.7	42	4	US-09-042-353-380	Sequence 380, App
558	16.8	0.7	48	3	US-08-987-867A-14	Sequence 14, Appl	C 631	16.6	0.7	42	4	US-08-758-417A-230	Sequence 230, Appl
559	16.8	0.7	50	1	US-08-123-936-379	Sequence 379, App	C 632	16.6	0.7	44	1	US-07-872-673B-23	Sequence 23, Appl
560	16.8	0.7	50	1	US-08-374-641-36	Sequence 36, Appl	C 633	16.6	0.7	44	1	US-08-681-935-12	Sequence 12, Appl
561	16.8	0.7	50	1	US-08-475-228A-379	Sequence 379, App	C 634	16.6	0.7	44	1	US-08-741-881-35	Sequence 35, Appl
562	16.8	0.7	50	3	US-08-482-080A-379	Sequence 379, App	C 635	16.6	0.7	44	1	US-08-739-158-35	Sequence 35, Appl
563	16.8	0.7	50	3	US-08-985-162-1727	Sequence 1727, Ap	C 636	16.6	0.7	44	2	US-08-739-167-35	Sequence 35, Appl
564	16.8	0.7	50	4	US-08-849-567A-66	Sequence 66, Appl	C 637	16.6	0.7	44	3	US-08-404-796-35	Sequence 35, Appl
565	16.8	0.7	50	4	US-09-354-947-379	Sequence 379, App	C 638	16.6	0.7	44	3	US-08-931-869-35	Sequence 35, Appl
566	16.8	0.7	50	4	PCT-US93-12388-379	Sequence 379, App	C 639	16.6	0.7	44	4	US-08-939-323-12	Sequence 12, Appl
567	16.8	0.7	50	4	US-08-435-529-7	Sequence 7, Appl1	C 640	16.6	0.7	44	4	US-09-350-399-35	Sequence 35, Appl
568	16.6	0.7	24	1	US-08-810-720-3	Sequence 10, Appl1	C 641	16.6	0.7	44	4	US-09-236-140A-35	Sequence 35, Appl
569	16.6	0.7	25	3	US-09-253-396A-10	Sequence 10, Appl1	C 642	16.6	0.7	44	4	US-09-415-784-58	Sequence 58, Appl
570	16.6	0.7	27	4	US-08-584-040-158	Sequence 158, App	C 643	16.6	0.7	44	4	US-09-415-785A-58	Sequence 58, Appl
571	16.6	0.7	32	1	US-08-442-542-48	Sequence 48, Appl	C 644	16.6	0.7	44	4	US-08-944-465-58	Sequence 58, Appl
572	16.6	0.7	32	3	US-08-974-180-27	Sequence 27, Appl	C 645	16.6	0.7	44	4	US-09-415-868-58	Sequence 58, Appl
573	16.6	0.7	32	3	US-08-765-469-48	Sequence 48, Appl	C 646	16.6	0.7	44	4	US-09-415-900-58	Sequence 58, Appl
574	16.6	0.7	33	3	US-08-364-339-19	Sequence 19, Appl	C 647	16.6	0.7	44	6	5242821-25	Patent No. 5242821
575	16.6	0.7	33	1	US-08-413-118-114	Sequence 114, App	C 648	16.6	0.7	45	3	US-08-329-799-72	Sequence 72, Appl
576	16.6	0.7	33	1	US-08-487-034-19	Sequence 19, Appl	C 649	16.6	0.7	45	3	US-08-834-314-2	Sequence 2, Appl1
577	16.6	0.7	33	2	US-08-975-902-46	Sequence 46, Appl	C 650	16.6	0.7	45	5	PCT-US96-00888-14	Sequence 14, Appl
578	16.6	0.7	33	2	US-08-360-606B-14	Sequence 26, Appl	C 651	16.6	0.7	46	4	US-09-641-638-1292	Sequence 1292, Ap
579	16.6	0.7	33	2	US-08-577-121-26	Sequence 26, Appl	C 652	16.6	0.7	47	2	US-08-936-387-8	Sequence 8, Appl
580	16.6	0.7	33	3	US-08-473-446-114	Sequence 114, App	C 653	16.6	0.7	47	2	US-08-883-795A-29	Sequence 29, Appl
581	16.6	0.7	33	3	US-08-810-720-4	Sequence 4, Appl1	C 654	16.6	0.7	47	2	US-08-883-795A-30	Sequence 30, Appl
582	16.6	0.7	33	3	US-09-251-565-46	Sequence 26, Appl	C 655	16.6	0.7	47	4	US-09-338-907-324	Sequence 324, App
583	16.6	0.7	33	3	US-08-985-700-26	Sequence 26, Appl	C 656	16.6	0.7	47	4	US-09-218-207-124	Sequence 38, Appl
584	16.6	0.7	33	4	US-09-411-977-29	Sequence 29, Appl	C 657	16.6	0.7	47	4	US-09-345-882-38	Sequence 743, App
585	16.6	0.7	33	4	PCT-US95-16916-26	Sequence 26, Appl	C 658	16.6	0.7	47	4	US-09-641-638-1032	Sequence 1032, App
586	16.6	0.7	34	1	US-08-270-985-18	Sequence 18, Appl	C 659	16.6	0.7	47	4	US-09-641-638-1079	Sequence 1079, Ap
587	16.6	0.7	34	2	US-08-479-733A-19	Sequence 19, Appl	C 660	16.6	0.7	47	4	US-09-641-638-1152	Sequence 1152, Ap
588	16.6	0.7	34	2	US-08-487-427-19	Sequence 19, Appl	C 661	16.6	0.7	47	4	US-08-616-133-13	Sequence 13, Appl
589	16.6	0.7	34	3	US-08-479-727A-19	Sequence 19, Appl	C 662	16.6	0.7	48	1	US-08-802-985-13	Sequence 13, Appl
590	16.6	0.7	34	3	US-08-478-208-27	Sequence 27, Appl	C 663	16.6	0.7	48	1	US-08-975-902-10	Sequence 40, Appl
591	16.6	0.7	34	3	US-08-482-369A-19	Sequence 19, Appl	C 664	16.6	0.7	48	2	US-08-845-161A-16	Sequence 16, Appl
592	16.6	0.7	34	3	US-09-009-217-25	Sequence 25, Appl	C 665	16.6	0.7	48	2	US-09-270-751-16	Sequence 16, Appl
593	16.6	0.7	34	3	PCT-US95-07439-19	Sequence 19, Appl	C 666	16.6	0.7	48	3	US-09-305-408-9	Sequence 9, Appl1
594	16.6	0.7	34	5	US-09-009-656-25	Sequence 25, Appl	C 667	16.6	0.7	48	4	US-08-692-610-9	Sequence 9, Appl1
595	16.6	0.7	35	4	US-09-386-607-8	Sequence 8, Appl1	C 668	16.6	0.7	49	1	US-08-682-471-8	Sequence 8, Appl1
596	16.6	0.7	35	4	US-08-235-836C-25	Sequence 25, Appl	C 669	16.6	0.7	49	1	US-08-683-124-9	Sequence 9, Appl1
597	16.6	0.7	35	2	US-08-669-721-1	Sequence 1, Appl1	C 670	16.6	0.7	49	1	US-09-538-709-1177	Sequence 9, Appl1
598	16.6	0.7	36	2	US-08-140-083A-4	Sequence 4, Appl1	C 671	16.6	0.7	49	1	US-08-171-389-162	Sequence 162, App
599	16.6	0.7	36	3	US-09-189-344-1	Sequence 1, Appl1	C 672	16.6	0.7	50	1	US-08-120-901-41	Sequence 41, Appl
600	16.6	0.7	36	3	US-08-387-315A-9	Sequence 9, Appl1	C 673	16.6	0.7	50	1	US-08-475-228A-562	Sequence 562, App
601	16.6	0.7	37	2	US-08-754-559-9	Sequence 2, Appl1	C 674	16.6	0.7	50	2	US-08-482-080A-562	Sequence 562, App
602	16.6	0.7	37	1	US-09-054-711C-2	Sequence 2, Appl1	C 675	16.6	0.7	50	2	US-09-354-947-562	Sequence 562, App
603	16.6	0.7	38	4	US-08-634-060-60	Sequence 60, Appl	C 676	16.6	0.7	50	3	PCT-US93-12388-562	Sequence 562, App
604	16.6	0.7	39	1	US-09-292-563-8	Sequence 8, Appl1	C 677	16.6	0.7	50	4	US-09-489-765A-36	Sequence 36, App
605	16.6	0.7	39	4	US-09-564-805-112	Sequence 112, App	C 678	16.6	0.7	50	4	US-08-060-925A-7	Sequence 7, Appl1
606	16.6	0.7	39	4	5256648-29	Sequence 11, Appl	C 679	16.4	0.7	26	1	US-08-758-306-724	Sequence 74, Appl1
607	16.6	0.7	40	2	US-08-281-423-11	Sequence 11, Appl	C 680	16.4	0.7	27	1	US-08-758-306-1120	Sequence 1120, Ap
608	16.6	0.7	40	2	US-08-281-423-17	Sequence 17, Appl	C 681	16.4	0.7	27	1		
609	16.6	0.7	40	2	US-08-281-423-17	Sequence 17, Appl	C 682	16.4	0.7	27	1		
610	16.6	0.7	40	2	US-08-281-423-17	Sequence 17, Appl	C 683	16.4	0.7	27	1		
611	16.6	0.7	40	4	US-08-748-547-16	Sequence 16, Appl	C 684	16.4	0.7	27	1		

C 685	16.4	0.7	27	3	US-08-985-162-1312	Sequence 1312, Ap	C 758	16.4	0.7	42	3	US-08-612-973-103	Sequence 103, App
686	16.4	0.7	27	4	US-08-985-162-1315	Sequence 1315, Ap	C 759	16.4	0.7	42	4	US-08-927-597-103	Sequence 103, App
C 687	16.4	0.7	27	4	US-08-584-040-192	Sequence 192, App	C 760	16.4	0.7	42	4	US-09-813-781-43	Sequence 43, App1
C 688	16.4	0.7	27	4	US-08-584-040-622	Sequence 622, App	C 761	16.4	0.7	42	5	PCT-US95-12414-8	Sequence 8, App1
C 689	16.4	0.7	27	4	US-08-584-040-1046	Sequence 1046, Ap	C 762	16.4	0.7	43	1	US-08-403-762a-18	Sequence 18, App1
C 690	16.4	0.7	30	2	US-08-632-470-16	Sequence 16, App1	C 763	16.4	0.7	43	1	US-08-403-762a-20	Sequence 20, App1
C 691	16.4	0.7	31	1	US-08-647-584-44	Sequence 44, App1	C 764	16.4	0.7	43	1	US-08-292-081a-13	Sequence 13, App1
C 692	16.4	0.7	33	4	US-09-191-852-10	Sequence 10, App1	C 765	16.4	0.7	43	2	US-08-752-495-13	Sequence 13, App1
C 693	16.4	0.7	33	4	US-08-817-906-10	Sequence 10, App1	C 766	16.4	0.7	43	4	US-09-387-800-5	Sequence 5, App1
C 694	16.4	0.7	33	5	PCT-US95-13376-10	Sequence 10, App1	C 767	16.4	0.7	43	4	US-09-363-939a-91	Sequence 91, App1
C 695	16.4	0.7	35	1	US-08-126-594-15	Sequence 15, App1	C 768	16.4	0.7	44	1	US-07-931-473b-110	Sequence 110, App
C 696	16.4	0.7	35	1	US-08-126-594-17	Sequence 17, App1	C 769	16.4	0.7	44	1	US-07-714-131c-110	Sequence 110, App
C 697	16.4	0.7	35	1	US-08-126-594-19	Sequence 19, App1	C 770	16.4	0.7	44	1	US-08-458-084-17	Sequence 17, App1
C 698	16.4	0.7	35	1	US-08-048-975-3	Sequence 3, App1	C 771	16.4	0.7	44	1	US-08-205-508-17	Sequence 17, App1
C 699	16.4	0.7	35	1	US-08-364-339-16	Sequence 16, App1	C 772	16.4	0.7	44	1	US-08-412-110-110	Sequence 110, App
C 700	16.4	0.7	35	1	US-08-465-811a-15	Sequence 15, App1	C 773	16.4	0.7	44	1	US-08-409-442a-110	Sequence 110, App
C 701	16.4	0.7	35	1	US-08-465-811a-17	Sequence 17, App1	C 774	16.4	0.7	44	2	US-08-469-609a-110	Sequence 110, App
C 702	16.4	0.7	35	1	US-08-487-034-16	Sequence 16, App1	C 775	16.4	0.7	44	3	US-09-143-190-110	Sequence 110, App
C 703	16.4	0.7	35	2	US-08-487-034-16	Sequence 16, App1	C 776	16.4	0.7	44	4	US-09-502-344-110	Sequence 110, App
C 704	16.4	0.7	35	2	US-08-619-542b-15	Sequence 15, App1	C 777	16.4	0.7	44	5	PCT-US95-02945-17	Sequence 17, App1
C 705	16.4	0.7	35	2	US-08-619-542b-17	Sequence 17, App1	C 778	16.4	0.7	45	1	US-07-885-689a-10	Sequence 10, App1
C 706	16.4	0.7	35	2	US-08-619-542b-19	Sequence 19, App1	C 779	16.4	0.7	45	1	US-08-219-4770-6	Sequence 6, App1
C 707	16.4	0.7	35	2	US-08-479-733a-6	Sequence 6, App1	C 780	16.4	0.7	45	1	US-08-197-770-6	Sequence 6, App1
C 708	16.4	0.7	35	2	US-08-405-373c-2	Sequence 2, App1	C 781	16.4	0.7	45	1	US-08-197-770-8	Sequence 8, App1
C 709	16.4	0.7	35	3	US-08-577-121-23	Sequence 23, App1	C 782	16.4	0.7	45	1	US-08-171-389-61	Sequence 61, App1
C 710	16.4	0.7	35	3	US-08-487-427-6	Sequence 6, App1	C 783	16.4	0.7	45	1	US-08-148-022-2	Sequence 2, App1
C 711	16.4	0.7	35	3	US-08-479-727a-6	Sequence 6, App1	C 784	16.4	0.7	45	1	US-08-476-685d-4	Sequence 4, App1
C 712	16.4	0.7	35	3	US-08-482-369a-6	Sequence 6, App1	C 785	16.4	0.7	45	1	US-07-854-603-31	Sequence 31, App1
C 713	16.4	0.7	35	4	US-08-985-700-23	Sequence 23, App1	C 786	16.4	0.7	45	1	US-08-123-936-61	Sequence 61, App1
C 714	16.4	0.7	35	4	US-09-168-738a-26	Sequence 26, App1	C 787	16.4	0.7	45	1	US-08-472-877b-4	Sequence 4, App1
C 715	16.4	0.7	35	4	US-09-940-019-26	Sequence 26, App1	C 788	16.4	0.7	45	2	US-08-451-822a-10	Sequence 10, App1
C 716	16.4	0.7	35	5	PCT-US95-07439-6	Sequence 6, App1	C 789	16.4	0.7	45	2	US-08-451-822a-61	Sequence 61, App1
C 717	16.4	0.7	35	5	PCT-US95-16916-23	Sequence 23, App1	C 790	16.4	0.7	45	3	US-08-482-080a-61	Sequence 61, App1
C 718	16.4	0.7	36	2	US-08-292-620a-1382	Sequence 1382, Ap	C 791	16.4	0.7	45	4	US-09-072-958-4	Sequence 4, App1
C 719	16.4	0.7	36	2	US-08-471-371-3	Sequence 3, App1	C 792	16.4	0.7	45	4	US-08-323-430-10	Sequence 10, App1
C 720	16.4	0.7	36	2	US-08-444-644-13	Sequence 13, App1	C 793	16.4	0.7	45	4	US-09-293-505-21	Sequence 21, App1
C 721	16.4	0.7	36	3	US-09-071-845-1382	Sequence 1382, Ap	C 794	16.4	0.7	45	4	US-09-354-947-61	Sequence 61, App1
C 722	16.4	0.7	36	3	US-09-071-845-1444	Sequence 1444, Ap	C 795	16.4	0.7	45	4	PCT-US93-12388-61	Sequence 61, App1
C 723	16.4	0.7	36	3	US-08-358-627f-24	Sequence 24, App1	C 796	16.4	0.7	45	5	PCT-US95-14639-8	Sequence 8, App1
C 724	16.4	0.7	36	4	US-08-450-962-9	Sequence 9, App1	C 797	16.4	0.7	45	5	US-08-663-688a-4	Sequence 4, App1
C 725	16.4	0.7	36	4	US-09-219-797-5	Sequence 13, App1	C 798	16.4	0.7	46	2	US-08-191-160-25	Sequence 25, App1
C 726	16.4	0.7	36	4	US-08-465-712c-24	Sequence 24, App1	C 799	16.4	0.7	46	4	US-08-850-049-103	Sequence 103, App
C 727	16.4	0.7	36	4	US-09-552-733-24	Sequence 24, App1	C 800	16.4	0.7	47	2	US-09-641-638-823	Sequence 823, App
C 728	16.4	0.7	36	4	US-09-552-733-45	Sequence 45, App1	C 801	16.4	0.7	47	4	US-09-641-638-1181	Sequence 1181, Ap
C 729	16.4	0.7	38	4	US-08-469-260a-146	Sequence 146, App	C 802	16.4	0.7	47	4	US-09-641-638-1181	Sequence 1181, Ap
C 730	16.4	0.7	38	4	US-07-931-473b-146	Sequence 146, App	C 803	16.4	0.7	47	4	US-09-641-638-1181	Sequence 1181, Ap
C 731	16.4	0.7	38	4	US-07-931-473b-146	Sequence 146, App	C 804	16.4	0.7	47	4	US-09-641-638-1181	Sequence 1181, Ap
C 732	16.4	0.7	39	1	US-08-412-110-146	Sequence 146, App	C 805	16.4	0.7	47	4	US-09-641-638-1181	Sequence 1181, Ap
C 733	16.4	0.7	39	1	US-08-409-442a-146	Sequence 146, App	C 806	16.4	0.7	47	4	US-09-641-638-1181	Sequence 1181, Ap
C 734	16.4	0.7	39	1	US-08-409-442a-146	Sequence 146, App	C 807	16.4	0.7	47	4	US-09-641-638-1181	Sequence 1181, Ap
C 735	16.4	0.7	39	1	US-08-409-442a-146	Sequence 146, App	C 808	16.4	0.7	47	4	US-09-641-638-1181	Sequence 1181, Ap
C 736	16.4	0.7	39	2	US-09-235-246-17	Sequence 17, App1	C 809	16.4	0.7	47	4	US-09-641-638-1181	Sequence 1181, Ap
C 737	16.4	0.7	39	3	US-09-235-246-17	Sequence 17, App1	C 810	16.4	0.7	47	4	US-09-641-638-1181	Sequence 1181, Ap
C 738	16.4	0.7	39	3	US-09-143-190-146	Sequence 146, App	C 811	16.4	0.7	48	1	US-08-177-502-5	Sequence 5, App1
C 739	16.4	0.7	39	4	US-09-517-871-16	Sequence 16, App1	C 812	16.4	0.7	48	1	US-08-639-763-11	Sequence 11, App1
C 740	16.4	0.7	40	4	US-08-199-507b-46	Sequence 46, App1	C 813	16.4	0.7	48	1	US-08-783-275-6	Sequence 6, App1
C 741	16.4	0.7	40	1	US-08-441-828-46	Sequence 46, App1	C 814	16.4	0.7	48	1	US-08-727-708-6	Sequence 6, App1
C 742	16.4	0.7	40	1	US-08-040-548-58	Sequence 58, App1	C 815	16.4	0.7	48	2	US-08-383-621-8	Sequence 8, App1
C 743	16.4	0.7	40	1	US-08-466-344-58	Sequence 58, App1	C 816	16.4	0.7	48	3	US-08-459-906-8	Sequence 8, App1
C 744	16.4	0.7	40	2	US-08-867-941-61	Sequence 61, App1	C 817	16.4	0.7	48	3	US-08-789-333b-66	Sequence 66, App1
C 745	16.4	0.7	40	2	US-09-074-658-61	Sequence 61, App1	C 818	16.4	0.7	48	3	US-08-789-333b-66	Sequence 66, App1
C 746	16.4	0.7	40	4	US-09-313-221a-71	Sequence 71, App1	C 819	16.4	0.7	48	4	US-09-367-206-9	Sequence 9, App1
C 747	16.4	0.7	40	4	US-08-357-698-2	Sequence 2, App1	C 820	16.4	0.7	48	4	US-08-787-738b-66	Sequence 66, App1
C 748	16.4	0.7	41	1	US-08-935-855-16	Sequence 16, App1	C 821	16.4	0.7	48	6	5240847-32	Patent No. 5240847
C 749	16.4	0.7	41	2	PCT-US93-12682-2	Sequence 2, App1	C 822	16.4	0.7	49	2	US-08-588-983-30	Sequence 30, App1
C 750	16.4	0.7	41	5	US-08-466-303-8	Sequence 8, App1	C 823	16.4	0.7	49	2	US-08-588-983-30	Sequence 30, App1
C 751	16.4	0.7	41	5	US-08-466-303-8	Sequence 8, App1	C 824	16.4	0.7	49	4	US-09-400-541-10	Sequence 10, App1
C 752	16.4	0.7	42	1	US-08-314-503a-8	Sequence 8, App1	C 825	16.4	0.7	49	4	US-09-367-206-35	Sequence 35, App1
C 753	16.4	0.7	42	1	US-08-468-066-8	Sequence 8, App1	C 826	16.4	0.7	49	4	US-08-899-999-10	Sequence 10, App1
C 754	16.4	0.7	42	1	US-08-468-066-8	Sequence 8, App1	C 827	16.4	0.7	50	1	US-08-171-389-378	Sequence 378, App
C 755	16.4	0.7	42	2	US-08-466-337-1	Sequence 1, App1	C 828	16.4	0.7	50	1	US-08-171-389-378	Sequence 378, App
C 756	16.4	0.7	42	3	US-08-836-337-1	Sequence 1, App1	C 829	16.4	0.7	50	1	US-08-324-001-10	Sequence 10, App1
C 757	16.4	0.7	42	3	US-08-466-743-8	Sequence 8, App1	C 830	16.4	0.7	50	1	US-08-324-001-11	Sequence 11, App1

C 831	16.4	0.7	50	1	US-08-471-206-26	Sequence 26, Appl	C 904	16.2	0.7	38	2	US-08-292-620A-2126	Sequence 2126, Ap
C 832	16.4	0.7	50	1	US-08-123-936-378	Sequence 378, App	C 905	16.2	0.7	38	2	US-08-292-620A-2307	Sequence 2307, Ap
C 833	16.4	0.7	50	1	US-08-123-936-599	Sequence 599, App	C 906	16.2	0.7	38	2	US-08-857-946-51	Sequence 51, Appl
C 834	16.4	0.7	50	2	US-08-828-007-7	Sequence 7, Appl	C 907	16.2	0.7	38	3	US-08-970-740-51	Sequence 51, Appl
C 835	16.4	0.7	50	2	US-08-475-228A-378	Sequence 378, App	C 908	16.2	0.7	38	3	US-09-071-845-2126	Sequence 2126, Ap
C 836	16.4	0.7	50	2	US-08-475-228A-599	Sequence 599, App	C 909	16.2	0.7	38	3	US-09-071-845-2307	Sequence 2307, Ap
C 837	16.4	0.7	50	2	US-08-483-468-2	Sequence 2, Appl	C 910	16.2	0.7	38	4	US-09-232-479-24	Sequence 24, Appl
C 838	16.4	0.7	50	3	US-08-482-080A-378	Sequence 378, App	C 911	16.2	0.7	38	4	US-09-784-990-24	Sequence 24, Appl
C 839	16.4	0.7	50	3	US-08-482-080A-599	Sequence 599, App	C 912	16.2	0.7	39	1	US-08-331-398A-4	Sequence 4, Appl
C 840	16.4	0.7	50	3	US-08-985-162-1669	Sequence 1669, Ap	C 913	16.2	0.7	39	1	US-08-469-665-5	Sequence 5, Appl
C 841	16.4	0.7	50	4	US-09-354-947-378	Sequence 378, App	C 914	16.2	0.7	39	1	US-08-451-715A-58	Sequence 58, Appl
C 842	16.4	0.7	50	4	US-09-354-947-599	Sequence 599, App	C 915	16.2	0.7	39	2	US-08-417-210A-132	Sequence 132, App
C 843	16.4	0.7	50	5	PCT-US93-12388-378	Sequence 378, App	C 916	16.2	0.7	39	2	US-09-038-596-5	Sequence 5, Appl
C 844	16.4	0.7	50	5	PCT-US93-12388-599	Sequence 599, App	C 917	16.2	0.7	39	2	US-08-331-397B-4	Sequence 4, Appl
C 845	16.2	0.7	24	2	US-08-632-575B-25	Sequence 25, Appl	C 918	16.2	0.7	39	2	US-08-759-804A-4	Sequence 4, Appl
C 846	16.2	0.7	27	1	US-07-910-222B-3	Sequence 1, Appl	C 919	16.2	0.7	39	4	US-09-227-693-3	Sequence 4, Appl
C 847	16.2	0.7	27	1	US-07-910-222B-3	Sequence 1, Appl	C 920	16.2	0.7	39	4	US-08-860-038-23	Sequence 23, Appl
C 848	16.2	0.7	27	1	US-08-070-158-2	Sequence 2, Appl	C 921	16.2	0.7	39	4	US-09-580-923-23	Sequence 23, Appl
C 849	16.2	0.7	27	1	US-08-200-716-1	Sequence 1, Appl	C 922	16.2	0.7	39	5	PCT-US95-00421-5	Sequence 5, Appl
C 850	16.2	0.7	27	1	US-08-200-716-3	Sequence 3, Appl	C 923	16.2	0.7	40	1	US-08-443-957-10	Sequence 10, Appl
C 851	16.2	0.7	27	2	US-08-015-147-1	Sequence 1, Appl	C 924	16.2	0.7	40	4	US-09-091-814-85	Sequence 85, Appl
C 852	16.2	0.7	27	2	US-08-015-147-3	Sequence 3, Appl	C 925	16.2	0.7	40	4	US-09-189-462-25	Sequence 25, Appl
C 853	16.2	0.7	27	2	US-08-482-651-55	Sequence 55, Appl	C 926	16.2	0.7	40	4	US-09-189-462-26	Sequence 26, Appl
C 854	16.2	0.7	27	3	US-08-469-015-2	Sequence 2, Appl	C 927	16.2	0.7	41	1	US-08-480-525-5	Sequence 3, Appl
C 855	16.2	0.7	27	3	US-08-463-893-2	Sequence 2, Appl	C 928	16.2	0.7	41	3	US-08-477-934-28	Sequence 28, Appl
C 856	16.2	0.7	27	4	US-08-660-092-209	Sequence 209, App	C 929	16.2	0.7	41	4	US-09-233-086-47	Sequence 47, Appl
C 857	16.2	0.7	27	4	US-09-358-972-99	Sequence 99, Appl	C 930	16.2	0.7	41	4	US-07-986-776A-28	Sequence 28, Appl
C 858	16.2	0.7	27	4	US-09-504-505-2	Sequence 2, Appl	C 931	16.2	0.7	41	5	PCT-US94-06422-3	Sequence 3, Appl
C 859	16.2	0.7	27	4	US-08-980-241-1	Sequence 1, Appl	C 932	16.2	0.7	42	1	US-08-391-000-34	Sequence 34, Appl
C 860	16.2	0.7	27	4	US-09-160-513-209	Sequence 209, App	C 933	16.2	0.7	42	2	US-08-741-931-34	Sequence 34, Appl
C 861	16.2	0.7	30	1	US-08-347-792-21	Sequence 21, Appl	C 934	16.2	0.7	42	2	US-08-956-047-18	Sequence 18, Appl
C 862	16.2	0.7	30	1	US-08-431-357-21	Sequence 21, Appl	C 935	16.2	0.7	42	3	US-08-480-640A-120	Sequence 120, App
C 863	16.2	0.7	30	2	US-08-454-557C-6	Sequence 6, Appl	C 936	16.2	0.7	42	3	US-08-962-503-1	Sequence 1, Appl
C 864	16.2	0.7	30	2	US-08-340-426D-6	Sequence 6, Appl	C 937	16.2	0.7	42	3	US-08-295-802-120	Sequence 120, App
C 865	16.2	0.7	30	2	US-08-450-673C-6	Sequence 6, Appl	C 938	16.2	0.7	42	4	US-08-488-237A-120	Sequence 120, App
C 866	16.2	0.7	30	2	US-08-642-406A-14	Sequence 14, Appl	C 939	16.2	0.7	42	4	US-08-375-992A-120	Sequence 120, App
C 867	16.2	0.7	30	3	US-08-434-000A-16	Sequence 16, Appl	C 940	16.2	0.7	43	1	US-08-473-096-1	Sequence 1, Appl
C 868	16.2	0.7	30	3	US-08-961-083-417	Sequence 417, App	C 941	16.2	0.7	43	3	US-08-934-694-11	Sequence 11, Appl
C 869	16.2	0.7	30	4	US-09-312-157-16	Sequence 16, Appl	C 942	16.2	0.7	43	3	US-09-143-068-11	Sequence 11, Appl
C 870	16.2	0.7	30	4	US-09-199-534-14	Sequence 14, Appl	C 943	16.2	0.7	43	4	US-08-906-156A-81	Sequence 81, Appl
C 871	16.2	0.7	30	4	US-08-956-653A-38	Sequence 38, Appl	C 944	16.2	0.7	43	4	US-09-143-707-11	Sequence 11, Appl
C 872	16.2	0.7	30	4	US-08-327-874A-31	Sequence 31, Appl	C 945	16.2	0.7	43	4	US-09-202-089-11	Sequence 11, Appl
C 873	16.2	0.7	30	4	US-09-199-534-14	Sequence 14, Appl	C 946	16.2	0.7	43	4	US-09-511-133-11	Sequence 11, Appl
C 874	16.2	0.7	30	5	PCT-US94-09700-31	Sequence 31, Appl	C 947	16.2	0.7	43	4	US-09-690-169-11	Sequence 11, Appl
C 875	16.2	0.7	30	5	PCT-US95-15353-21	Sequence 21, Appl	C 948	16.2	0.7	43	4	US-09-511-631-11	Sequence 11, Appl
C 876	16.2	0.7	30	5	PCT-US95-17111A-6	Sequence 6, Appl	C 949	16.2	0.7	44	1	US-08-171-389-2	Sequence 2, Appl
C 877	16.2	0.7	32	1	US-08-239-889A-2	Sequence 2, Appl	C 950	16.2	0.7	44	1	US-08-123-936-2	Sequence 2, Appl
C 878	16.2	0.7	32	2	US-08-889-909A-20	Sequence 20, Appl	C 951	16.2	0.7	44	2	US-08-475-228A-2	Sequence 2, Appl
C 879	16.2	0.7	32	2	US-09-073-395-4	Sequence 4, Appl	C 952	16.2	0.7	44	3	US-08-482-080A-2	Sequence 2, Appl
C 880	16.2	0.7	32	4	US-09-156-163A-20	Sequence 20, Appl	C 953	16.2	0.7	44	4	US-09-354-947-2	Sequence 2, Appl
C 881	16.2	0.7	32	5	PCT-US95-05659-2	Sequence 2, Appl	C 954	16.2	0.7	44	5	PCT-US93-12388-2	Sequence 2, Appl
C 882	16.2	0.7	33	3	US-08-711-218-9	Sequence 9, Appl	C 955	16.2	0.7	45	1	US-08-411-795B-173	Sequence 173, App
C 883	16.2	0.7	33	3	US-08-726-807B-11	Sequence 11, Appl	C 956	16.2	0.7	45	1	US-08-469-319A-173	Sequence 173, App
C 884	16.2	0.7	33	3	US-09-258-367-11	Sequence 11, Appl	C 957	16.2	0.7	45	2	US-08-975-902-33	Sequence 33, Appl
C 885	16.2	0.7	33	3	US-08-454-928-3	Sequence 3, Appl	C 958	16.2	0.7	45	2	US-08-560-098A-25	Sequence 25, Appl
C 886	16.2	0.7	33	4	US-09-546-550-11	Sequence 11, Appl	C 959	16.2	0.7	45	3	US-09-251-365-33	Sequence 33, Appl
C 887	16.2	0.7	33	4	US-09-431-414-11	Sequence 11, Appl	C 960	16.2	0.7	45	4	US-08-764-419-173	Sequence 173, App
C 888	16.2	0.7	33	4	US-09-225-670-11	Sequence 11, Appl	C 961	16.2	0.7	45	4	US-08-469-419-173	Sequence 173, App
C 889	16.2	0.7	33	4	US-09-431-349C-11	Sequence 11, Appl	C 962	16.2	0.7	46	1	US-08-171-389-146	Sequence 146, App
C 890	16.2	0.7	35	1	US-08-361-337-60	Sequence 60, Appl	C 963	16.2	0.7	46	1	US-08-123-936-146	Sequence 146, App
C 891	16.2	0.7	35	1	US-08-399-696-69	Sequence 69, Appl	C 964	16.2	0.7	46	2	US-08-475-228A-146	Sequence 146, App
C 892	16.2	0.7	35	4	US-09-597-877-22	Sequence 22, Appl	C 965	16.2	0.7	46	3	US-08-482-080A-3	Sequence 3, Appl
C 893	16.2	0.7	36	1	US-08-435-350-19	Sequence 19, Appl	C 966	16.2	0.7	46	4	US-09-406-074-3	Sequence 3, Appl
C 894	16.2	0.7	36	2	US-08-140-083A-3	Sequence 3, Appl	C 967	16.2	0.7	46	4	US-09-354-947-146	Sequence 146, App
C 895	16.2	0.7	36	2	US-08-455-968B-42	Sequence 42, Appl	C 968	16.2	0.7	46	4	US-09-345-882-60	Sequence 60, Appl
C 896	16.2	0.7	36	3	US-08-781-891-198	Sequence 198, App	C 969	16.2	0.7	46	4	US-09-641-638B-333	Sequence 833, App
C 897	16.2	0.7	37	1	US-08-264-115-5	Sequence 5, Appl	C 970	16.2	0.7	46	4	US-09-313-221A-16	Sequence 16, App
C 898	16.2	0.7	37	1	US-08-387-315A-9	Sequence 9, Appl	C 971	16.2	0.7	46	5	PCT-US93-12388-146	Sequence 146, App
C 899	16.2	0.7	37	1	US-08-294-424-42	Sequence 42, Appl	C 972	16.2	0.7	47	1	US-08-171-389-165	Sequence 165, App
C 900	16.2	0.7	37	2	US-08-754-559-9	Sequence 9, Appl	C 973	16.2	0.7	47	1	US-08-123-936-165	Sequence 165, App
C 901	16.2	0.7	37	4	US-08-398-590A-50	Sequence 50, Appl	C 974	16.2	0.7	47	2	US-08-475-228A-165	Sequence 165, App
C 902	16.2	0.7	37	4	US-08-894-997-52	Sequence 52, Appl	C 975	16.2	0.7	47	2	US-08-553-257A-5	Sequence 5, Appl
C 903	16.2	0.7	38	1	US-08-441-714-2	Sequence 2, Appl	C 976	16.2	0.7	47	3	US-08-482-080A-165	Sequence 165, App

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980 16.2 0.7 47 4 US-09-190-911-8
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C 994 16.2 0.7 48 1 US-08-171-389-19
C 995 16.2 0.7 48 1 US-08-391-000-2
C 996 16.2 0.7 48 1 US-08-123-936-19
C 997 16.2 0.7 48 2 US-08-169-948B-38
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C1000 16.2 0.7 48 2 US-08-448-873-38

ALIGNMENTS

Sequence 8, Appl
Sequence 210, App
Sequence 210, App
Sequence 8, Appl
Sequence 165, App
Sequence 48, Appl
Sequence 54, Appl
Sequence 839, App
Sequence 840, App
Sequence 1167, Ap
Sequence 1219, Ap
Sequence 1231, Ap
Sequence 165, App
Sequence 35, Appl
Sequence 64, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 2, Appl
Sequence 19, Appl
Sequence 38, Appl
Sequence 19, Appl
Sequence 38, Appl
Sequence 38, Appl

RESULT 1
US-08-859-998-1322/C
Sequence 1322, Application US/08859998
Patent No. 5994076
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Bibilashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,998
FILING DATE: 21-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 1322:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

FEATURE:
OTHER INFORMATION: oligonucleotide primer
US-08-859-998-1322

Query Match 1.2%; Score 28; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 859 CTTGAGTCTCAGTGTGATGACCCACAC 886
Db 28 CTTGAGTCTCAGTGTGATGACCCACAC 1

RESULT 2

US-09-225-928-1322/C
Sequence 1322, Application US/09225928
Patent No. 6352829

GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Bibilashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,928
FILING DATE: 05-Jan-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,998
FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 1322:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
SEQUENCE DESCRIPTION: SEQ ID NO: 1322:

Query Match 1.2%; Score 28; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 859 CTTGAGTCTCAGTGTGATGACCCACAC 886
Db 28 CTTGAGTCTCAGTGTGATGACCCACAC 1

RESULT 3
US-09-382-155-37

Sequence 37, Application US/09382155B
Patent No. 6160095
GENERAL INFORMATION:
APPLICANT: CHAUDHARY, PREET M
TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-KB, JNK AND APOPTOSIS
TITLE OF INVENTION: PATHWAYS AND METHODS OF USING THE SAME
FILE REFERENCE: Chaudhary
CURRENT APPLICATION NUMBER: US/09/382,155B
CURRENT FILING DATE: 1999-08-24
EARLIER APPLICATION NUMBER: 09/074,044
EARLIER FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 37
LENGTH: 29
TYPE: DNA
ORGANISM: Homo sapiens
US-09-382-155-37

Query Match 1.2%; Score 27.4; DB 4; Length 29;
Best Local Similarity 96.6%; Pred. No. 56;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 585 TCTTCATTGAGCTTGGCCGAGGACCGAG 613
|||||
DB 1 TCTTCATTGAGCTTGGCCGAGGACCGAG 29

RESULT 4
US-09-382-155-38/C
Sequence 38, Application US/09382155B
Patent No. 6160095
GENERAL INFORMATION:
APPLICANT: CHAUDHARY, PREET M
TITLE OF INVENTION: PROTEINS CAPABLE OF REGULATING NF-KB, JNK AND APOPTOSIS
TITLE OF INVENTION: PATHWAYS AND METHODS OF USING THE SAME
FILE REFERENCE: Chaudhary
CURRENT APPLICATION NUMBER: US/09/382,155B
CURRENT FILING DATE: 1999-08-24
EARLIER APPLICATION NUMBER: 09/074,044
EARLIER FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 38
LENGTH: 29
TYPE: DNA
ORGANISM: Homo sapiens
US-09-382-155-38

Query Match 1.2%; Score 27.4; DB 4; Length 29;
Best Local Similarity 96.6%; Pred. No. 56;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 585 TCTTCATTGAGCTTGGCCGAGGACCGAG 613
|||||
DB 29 TCTTCATTGAGCTTGGCCGAGGACCGAG 1

RESULT 5
US-08-859-998-1226/C
Sequence 1226, Application US/08859998
Patent No. 5994076
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Bibilashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.

STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,998
FILING DATE: 21-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 1226:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
US-08-859-998-1226

Query Match 1.2%; Score 27; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1812 TCTCAGCTATCTGCGCTCAGATCTTC 1838
|||||
DB 27 TCTCAGCTATCTGCGCTCAGATCTTC 1

RESULT 6
US-09-225-928-1226/C
Sequence 1226, Application US/09225928
Patent No. 6352829
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Bibilashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,928
FILING DATE: 05-Jan-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,998

FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 1226:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
US-09-225-928-1226
SEQUENCE DESCRIPTION: SEQ ID NO: 1226:

Query Match 1.1%; Score 27; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1812 TTCTACCTATCTGCGCTCACAATCTTC 1838
|||||
Db 27 TTCTACCTATCTGCGCTCACAATCTTC 1

RESULT 7
US-08-859-998-1225
Sequence 1225, Application US/08859998
Patent No. 5994076
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Bibilashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859, 998
FILING DATE: 21-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 1225:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

FEATURE:
OTHER INFORMATION: oligonucleotide primer
US-08-859-998-1225

Query Match 1.1%; Score 26; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1605 TGTACCACACCCAGGCGTATGAGA 1630
|||||
Db 1 TTGTACCACACCCAGGCGTATGAGA 26

RESULT 8
US-08-859-998-1321
Sequence 1321, Application US/08859998
Patent No. 5994076
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Bibilashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859, 998
FILING DATE: 21-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 1321:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
US-08-859-998-1321

Query Match 1.1%; Score 26; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 584 TTCTCATTCAGGCTTGCCGAGGAGC 609
|||||
Db 1 TTCTCATTCAGGCTTGCCGAGGAGC 26

RESULT 9
US-09-225-928-1225
Sequence 1225, Application US/09225928

```

Patent No. 6352829
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
Jokhadze, George
Biblashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,928
FILING DATE: 05-Jan-1999
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,998
FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 1225:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
SEQUENCE DESCRIPTION: SEQ ID NO: 1225:
US-09-225-928-1225
Query Match 1.1%; Score 26; DB 4; Length 26
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels
0
Cy 1605 TGTATCCACACCCAGGCTATGAGA 1630
|||||
Db 1 TGTATCCACACCCAGGCTATGAGA 26
|||||
RESULT 10
US-09-225-928-1321
Sequence 1321, Application US/09225928
Patent No. 6352829
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
Jokhadze, George
Biblashvili, Robert
TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025

```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/225,928
FILING DATE: 05-Jan-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,998
FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
REFERENCE/DOCKET NUMBER: 09096/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO: 1321:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
SEQUENCE DESCRIPTION: SEQ ID NO: 1321:
US-09-225-928-1321

Query Match          1.1%; Score 26; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 1,4e+02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      584 TTCTTCATCAGCGCTTGCCGAGGGAC 609
        |||||||
Db       1 TTTCTCATCAGCGCTTGC CGAGGAC 26

RESULT 11
US-09-171-162B-11
Sequence 11, Application US/09171162B
Patent No. 6432701
GENERAL INFORMATION:
APPLICANT: Mallett, Jacques
APPLICANT: Meloni, Rolando
APPLICANT: Ravassard, Philippe
APPLICANT: Trellhou, Fabienne
TITLE OF INVENTION: Derived Tyrosine Hydroxylase Gene Expression System
FILE REFERENCE: ST96018
CURRENT APPLICATION NUMBER: US/09/171,162B
CURRENT FILING DATE: 1998-10-14
PRIOR APPLICATION NUMBER: PCT/FR97/00636
PRIOR FILING DATE: 1997-10-04
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 41
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: oligo derived from HUMTH01
US-09-171-162B-11

Query Match          1.0%; Score 22.8; DB 4; Length 41;
Best Local Similarity 79.4%; Pred. No. 1.6e+03;
Matches 27; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1978 CTCACAAATTATTCATTCATCAATTATTAATTT 2011
        |||||
Db       3 CTCATCATTCATTCATTCATTCATTCATTCATTT 36

```


PRIOR APPLICATION NUMBER: 09/358,972
PRIOR FILING DATE: 1999-07-21
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patentln Ver. 2.1
SEQ ID NO 44
LENGTH: 48
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: TPOX allele
US-09-383-316-44

Query Match 0.9%; Score 21.2; DB 4; Length 48;
Best Local Similarity 69.0%; Pred. No. 5.1e+03;
Matches 29; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1985 ATTATCATCATCATCATTTATTCATGGTTCGACATAGT 2026
DB 45 ATTATCATCATCATCATTCATTCATTCAGGAGGTTCCCTAGT 4

RESULT 21
US-08-556-627A-7/C
Sequence 7, Application US/08556627A
Patent No. 6462175
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandes-Alnemri, Teresa
APPLICANT: Litwack, Gerald
APPLICANT: Armstrong, Robert
APPLICANT: Tomaselli, Kevin
TITLE OF INVENTION: Mch3, A No. 6462175e1 Apoptotic Protease,
TITLE OF INVENTION: Nucleic Acids Encoding and Methods of Use
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556,627A
FILING DATE: 13-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 1813
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-556-627A-7

Query Match 0.9%; Score 21; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2156 AAGTGAGAGAGATTATGCG 2176
DB 21 AAGTGAGAGAGATTATGCG 1

RESULT 22
US-09-564-805-130/C
Sequence 130, Application US/09564805
Patent No. 6333403
GENERAL INFORMATION:
APPLICANT: Tavtigian, Sean V.
APPLICANT: Teng, David H.F.
APPLICANT: Simard, Jacques
APPLICANT: Rommens, Johanna M.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
FILE REFERENCE: 2318-258
CURRENT APPLICATION NUMBER: US/09/564,805
CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/107,468
PRIOR FILING DATE: 1998-11-06
PRIOR APPLICATION NUMBER: 09/434,382
PRIOR FILING DATE: 1999-11-05
NUMBER OF SEQ ID NOS: 240
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 130
LENGTH: 41
TYPE: DNA
ORGANISM: Homo sapiens
US-09-564-805-130

Query Match 0.9%; Score 20.8; DB 4; Length 41;
Best Local Similarity 70.0%; Pred. No. 6.1e+03;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1231 CACAGAGAGACTTCTGAGAAAGCTCATGCTGTCC 1270
DB 41 CTACAGACACACTTTTGAAGATGGTCATAGCTGTTC 2

RESULT 23
US-08-400-864-1/C
Sequence 1, Application US/08400864
Patent No. 5721137
GENERAL INFORMATION:
APPLICANT: FRASCOTI, GIANNI
APPLICANT: GRANDI, GUIDO
TITLE OF INVENTION: PLASMID VECTOR AND ITS USE FOR THE
TITLE OF INVENTION: PRODUCTION OF HETEROLOGOUS PROTEINS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/400,864
FILING DATE: 08-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IT 000727 MI94A
FILING DATE: 15-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2264-083-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220


```
TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 49 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-400-864-1

Query Match
Best Local Similarity 64.6%; Pred. No. 6.8e+03;
Matches 31; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

OY 2068 AACCTGTAGCTTAAATATATCGACCTTTTACATTTCCA 2115
DB 49 AACCTATTTACATAAAATTTTCTCGAAGCAATAAATTTTCTA 2

RESULT 24
US-09-030-156-21/C
; Sequence 21, Application US/09030156
; Patent No. 6207373
; GENERAL INFORMATION:
; APPLICANT: Sosnowski, Ronald G.
; TITLE OF INVENTION: METHODS AND APPARATUS FOR DETERMINATION OF LENGTH
; FILE REFERENCE: DAVID B. MURPHY: Nanogen 221/157
; CURRENT APPLICATION NUMBER: US/09/030,156
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 21
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Human /
; OTHER INFORMATION: Biotin
US-09-030-156-21

Query Match
Best Local Similarity 0.9%; Score 20.6; DB 4; Length 41;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1985 ATTATCATTCATCATTTATTCATGGGTGC 2019
DB 40 ATTATTCATTCATTCATTCATTCAGTGGGTTTC 6

RESULT 25
US-09-645-757-21/C
; Sequence 21, Application US/09645757
; Patent No. 6395493
; GENERAL INFORMATION:
; APPLICANT: Sosnowski, Ronald G.
; TITLE OF INVENTION: METHODS AND APPARATUS FOR DETERMINATION OF LENGTH
; FILE REFERENCE: DAVID B. MURPHY: Nanogen 256/229
; CURRENT APPLICATION NUMBER: US/09/645,757
; CURRENT FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 21
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Human /
; OTHER INFORMATION: Biotin
US-09-645-757-21

Query Match
0.9%; Score 20.6; DB 4; Length 41;
Score 20.6; DB 4; Length 41;
```

```
Best Local Similarity 74.3%; Pred. No. 7e+03;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 1985 ATTATTCATTCATTCATTTATTCATGGGTGC 2019
DB 40 ATTATTCATTCATTCATTCATTCAGTGGGTTTC 6

RESULT 26
US-09-030-156-5
; Sequence 5, Application US/09030156
; Patent No. 6207373
; GENERAL INFORMATION:
; APPLICANT: Sosnowski, Ronald G.
; TITLE OF INVENTION: METHODS AND APPARATUS FOR DETERMINATION OF LENGTH
; FILE REFERENCE: DAVID B. MURPHY: Nanogen 221/157
; CURRENT APPLICATION NUMBER: US/09/030,156
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Human / Biotin
US-09-030-156-5

Query Match
Best Local Similarity 0.9%; Score 20.6; DB 4; Length 45;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1985 ATTATTCATTCATTCATTCATTTATTCAT 2011
DB 19 ATTATTCATTCATTCATTCATTCATTT 45

RESULT 27
US-09-645-757-5
; Sequence 5, Application US/09645757
; Patent No. 6395493
; GENERAL INFORMATION:
; APPLICANT: Sosnowski, Ronald G.
; TITLE OF INVENTION: METHODS AND APPARATUS FOR DETERMINATION OF LENGTH
; FILE REFERENCE: DAVID B. MURPHY: Nanogen 256/229
; CURRENT APPLICATION NUMBER: US/09/645,757
; CURRENT FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Human / Biotin
US-09-645-757-5

Query Match
Best Local Similarity 85.2%; Pred. No. 7.4e+03;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1985 ATTATTCATTCATTCATTCATTTATTCAT 2011
DB 19 ATTATTCATTCATTCATTCATTCATTT 45

RESULT 28
US-09-641-638-1284
; Sequence 1284, Application US/09641638
; Patent No. 6432648
; GENERAL INFORMATION:
```

APPLICANT: Blumenfeld, Marta
APPLICANT: Bougueleret, Lydie
APPLICANT: Chumakov, Ilya
APPLICANT: Cohen, Annick
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REFERENCE: GENSET.051CPI
CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patent.pm
SEQ ID NO 1284
LENGTH: 47
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 10-350-72 : polymorphic base C or T
US-09-641-638-1284

Query Match 0.9%; Score 20.2; DB 4; Length 47;
Best Local Similarity 75.8%; Pred. No. 1e+04;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy - 1670 ATCATCCAGAGAGAGCTGGAACCATGTGGGGC 1702
| | | | | | | | | | | | | | | | | | | | | |
Db 6 AGCATCAAGAGAGAGAGGCGCATGCTGGGTC 38

RESULT 29
US-07-828-444-7
Sequence 7, Application US/07828444
Patent No. 5290677
GENERAL INFORMATION:
APPLICANT: ROBERTSON, BETTY H.
APPLICANT: NAIMAN, OMANA V.
APPLICANT: BROWN, VICKI K.
APPLICANT: MARGOLIS, HAROLD S.
APPLICANT: KHANNA, BHAWNA
TITLE OF INVENTION: RAPID AND SENSITIVE TEST FOR DETECTING
TITLE OF INVENTION: HEPATITIS A VIRUS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1615 L STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/828,444
FILING DATE: 19920131
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: 5683/91979
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3067

TELEFAX: 202-822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-828-444-7

Query Match 0.9%; Score 20.2; DB 1; Length 50;
Best Local Similarity 75.8%; Pred. No. 1e+04;
Matches 25; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 501 AAGATGTCACACCAATTAAGATTGACAG 533
| | | | | | | | | | | | | | | | | | | | | |
Db 15 AAGTTGTATCACACAGTGAAGATCTTAAG 47

RESULT 30
US-08-863-639A-25/c
Sequence 25, Application US/08863639A
Patent No. 5981185
GENERAL INFORMATION:
APPLICANT: Matson, Robert S.
APPLICANT: Coassin, Peter J.
APPLICANT: Rampal, Jang B.
APPLICANT: Caskey, C. T.
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheldon & Mak
STREET: 225 South Lake Avenue, 9th Floor
CITY: Pasadena
STATE: CA
COUNTRY: USA
ZIP: 91101
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Corel WordPerfect 8 version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/863,639A
FILING DATE: May 28, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Joseph E. Muehl
REGISTRATION NUMBER: 20,532
REFERENCE/DOCKET NUMBER: 11859-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (626) 796-4000
TELEFAX: (626) 795-6321
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
US-08-863-639A-25

Query Match 0.9%; Score 20; DB 2; Length 36;
Best Local Similarity 72.2%; Pred. No. 9.6e+03;
Matches 26; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Oy 1892 GGAAGAGCAAGAGAGAGTGTAGCGAGAGAAGACAA 1927
| | | | | | | | | | | | | | | | | | | | | |
Db 36 GGAGAGAGAGAGAGAGAGAGAGAGAGAAGAGAAGAA 1

RESULT 31

US-08-938-830-31
; Sequence 31, Application US/08938830
; Patent No. 6040437
; GENERAL INFORMATION:
; APPLICANT: Lasky, Laurence A.
; APPLICANT: Dowbenko, Donald J.
; TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage
; TITLE OF INVENTION: Furrow-Associated Proteins (FSTPRs)
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/938,830
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/798419
; FILING DATE: 07-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1066P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; US-08-938-830-31
Query Match 0.9%; Score 20; DB 3; Length 42;
Best Local Similarity 72.2%; Pred. No. 1.1e+04;
Matches 26; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 777 TCTGCTCATCTGGAGGACGAGAAAGACCTGG 812
Db 5 TCGATCATGATGAGAGGTACGCGAAGAGCTGG 40
RESULT 32
US-09-641-638-1118
; Sequence 1118, Application US/09641638
; Patent No. 6432648
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bouguetelerc, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
; FILE REFERENCE: GENSET 051CPI
; CURRENT APPLICATION NUMBER: US/09/641,638
; CURRENT FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917

PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 1118
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 10-276-407 : polymorphic base C or T
US-09-641-638-1118
Query Match 0.9%; Score 20; DB 4; Length 47;
Best Local Similarity 76.7%; Pred. No. 1.1e+04;
Matches 23; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 1170 TCTCTTAAGATTATTTCTCTTTGTATG 1199
Db 2 TTACGTTATATATATTTCTCTCGAGTATG 31
RESULT 33
US-08-316-439A-31/C
; Sequence 31, Application US/08316439A
; Patent No. 5840520
; GENERAL INFORMATION:
; APPLICANT: CLARKE, DAVID KIRKWOOD
; APPLICANT: PABESE, PETER M
; TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS EXPRESSION
; TITLE OF INVENTION: SYSTEMS
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
; STREET: FIVE PALO ALTO SQUARE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,439A
; FILING DATE: September 30, 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/190,678
; FILING DATE: February 1, 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/925,061
; FILING DATE: August 4, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/527,237
; FILING DATE: May 22, 1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/399,728
; FILING DATE: August 28, 1989
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: CSERR, IOANN
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: AVIR-010/00US
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 843-5165
TELEFAX: (415) 857-0663
TELEX: 380816 COOLYX PA
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: SYNTHETIC DNA
US-08-316-439A-31

Query Match 0.9%; Score 20; DB 2; Length 50;
Best Local Similarity 65.9%; Pred. No. 1.2e+04;
Matches 29; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 2083 TAAATATATCTGGAACCTTTTATTCACAGCCTTATTT 2126
DB 48 TTAATTTAAGTGTAATTCATCAATCTTATTTGCCCATTTT 5

RESULT 34
US-09-276-533A-6/c
Sequence 6, Application US/09276533A
Patent No. 6436707
GENERAL INFORMATION:
APPLICANT: Zambrowicz, Brian
APPLICANT: Friedrich, Glenn A.
APPLICANT: Lilleberg, Stan
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: VECTORS FOR GENE MUTAGENESIS AND GENE
FILE REFERENCE: 07705-0006-00000
CURRENT APPLICATION NUMBER: US/09/276,533A
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: US 60/079,729
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: US 60/081,727
PRIOR FILING DATE: 1998-04-14
PRIOR APPLICATION NUMBER: US 60/109,302
PRIOR FILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 43
TYPE: DNA
ORGANISM: Mus musculus
US-09-276-533A-6

Query Match 0.9%; Score 19.8; DB 4; Length 43;
Best Local Similarity 69.2%; Pred. No. 1.2e+04;
Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 727 CTATTACTCGTGAGAGCCAGAGAGGCTCGTGT 765
DB 41 CTGTTGTCATGAGAGGAAGGACAGTACTGCTT 3

RESULT 35
US-09-158-863C-32/c
Sequence 32, Application US/09158863C
Patent No. 6280978
GENERAL INFORMATION:
APPLICANT: Mitchell, Lloyd G.
APPLICANT: Garcia-Blanco, Mariano A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR USE IN
SPLICING: SPLICESOME MEDIATED RNA TRANS-SPLICING
FILE REFERENCE: 31304-B-A
CURRENT APPLICATION NUMBER: US/09/158,863C
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 09/133,717
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: 09/087,233

PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 08/766,354
PRIOR FILING DATE: 1996-12-13
PRIOR APPLICATION NUMBER: 60/008,317
PRIOR FILING DATE: 1995-12-07
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 32
LENGTH: 47
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide primer complementary to the
US-09-158-863C-32

Query Match 0.9%; Score 19.8; DB 4; Length 47;
Best Local Similarity 63.8%; Pred. No. 1.3e+04;
Matches 30; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

OY 880 CCCACACTTCATGAGAGAGACAGATCCCTGTGTCTCCATGC 926
DB 47 CACCCAGTCCCATTTATGACGAGCGCCCTGACAGGTTACCATGC 1

RESULT 36
US-09-171-162B-13
Sequence 13, Application US/09171162B
Patent No. 6432701
GENERAL INFORMATION:
APPLICANT: Mallet, Jacques
APPLICANT: Meloni, Roland
APPLICANT: Ravassard, Philippe
APPLICANT: Treillhou, Fabienne
TITLE OF INVENTION: Derived Tyrosine Hydroxylase Gene Expression System
FILE REFERENCE: ST96018
CURRENT APPLICATION NUMBER: US/09/171,162B
PRIOR FILING DATE: 1998-10-14
PRIOR APPLICATION NUMBER: PCT/FR97/00636
PRIOR FILING DATE: 1997-10-04
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 31
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: oligo derived from HUMTHO1
US-09-171-162B-13

Query Match 0.8%; Score 19.6; DB 4; Length 31;
Best Local Similarity 84.6%; Pred. No. 1.1e+04;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1985 ATTATGCAATTCATTCATTCAT 2010
DB 6 ATTCATTCATTCATTCATTCATCAT 31

RESULT 37
PCT-US96-03916-35
Sequence 35, Application PC/TUS9603916
GENERAL INFORMATION:
APPLICANT: Wild, Martha A.
APPLICANT: Cochran, Mark D.
TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York

COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/03916
FILING DATE: 23-MAR-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126,597
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 39116-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US96-03916-35

Query Match 0.8%; Score 19.6; DB 5; Length 42;
Best Local Similarity 73.5%; Pred. No. 1.4e+04;
Matches 25; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1667 GGGATCATCCAGAGAGAGTGGACCATGATGGGG 1700
||||| 11111 111111111 1
Db 6 GGAATCCTCTAGACTGAGGAGGACCATGATGGG 39

RESULT 38
US-08-801-898A-27
Sequence 27, Application US/08801898A
Patent No. 5998602
GENERAL INFORMATION:
APPLICANT: Torrence, Paul F.
APPLICANT: Silverman, Robert H.
APPLICANT: Cirino, Nick M.
APPLICANT: Li, Guyling
APPLICANT: Xiao, Wei
TITLE OF INVENTION: RNAS E ACTIVATORS AND ANTISENSE
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennell & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,898A
FILING DATE: 18-FEB-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Polsant, Brian M.
REGISTRATION NUMBER: 28,462

REFERENCE/DOCKET NUMBER: 8656-009
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: Oligonucleotide
LOCATION: 1...49
OTHER INFORMATION: SPA4-antIRSV3'-3'(8251-8299)
US-08-801-898A-27

Query Match 0.8%; Score 19.6; DB 2; Length 49;
Best Local Similarity 66.7%; Pred. No. 1.5e+04;
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 2181 ATTTGGCATTGTTGTTTCAGATGCTTATCTTTGAAT 2222
||||| 11111 111111111 111111111 1
Db 7 ATTTGGTTGTTTGTATGAAATATAGTGTCTTTGATT 48

RESULT 39
US-08-556-627A-9/C
Sequence 9, Application US/08556627A
Patent No. 6462175
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandes-Alnemri, Teresa
APPLICANT: Litwack, Gerald
APPLICANT: Armstrong, Robert
APPLICANT: Tomaselli, Kevin
TITLE OF INVENTION: Mch3, A No. 6462175el Apoptotic Protease,
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556,627A
FILING DATE: 13-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 1813
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-556-627A-9

Query Match 0.8%; Score 19.4; DB 4; Length 21;
Best Local Similarity 95.2%; Pred. No. 1e+04;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 620 GATGCATCCAGCCGACGCG 640
 Db 21 GATGCATCCAGCCGACTAG 1

RESULT 40

US-08-231-342-17/c
 : Sequence 17, Application US/08231342
 : Patent No. 5827684

GENERAL INFORMATION:
 : APPLICANT: Sreekrishna, Kotikanyadanam
 : APPLICANT: Prevatt, William D
 : APPLICANT: Thill, Gregory P
 : APPLICANT: Davis, Geneva R
 : APPLICANT: Koutz, Patricia
 : APPLICANT: Bart, Kathryn A
 : APPLICANT: Hopkins, Sharon A
 : TITLE OF INVENTION: Production of Bacillus Entomotoxins in
 : TITLE OF INVENTION: Methylothrophic Yeast
 : NUMBER OF SEQUENCES: 27
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Fitch, Even, Tabin & Flannery
 : STREET: 135 S. LaSalle St.
 : CITY: Chicago
 : STATE: Illinois
 : COUNTRY: U.S.A.
 : ZIP: 60603-4277

COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentin Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/231.342
 : FILING DATE:
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US/07/926.448
 : FILING DATE:
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Feder, Scott B
 : REGISTRATION NUMBER: 33,129
 : REFERENCE/DOCKET NUMBER: 52627
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 312-372-7842
 : TELEFAX: 312-372-7848
 : INFORMATION FOR SEQ ID NO: 17:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 40 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: unknown
 : TOPOLOGY: unknown
 : MOLECULE TYPE: DNA (genomic)
 : US-08-231-342-17

Query Match 0.8%; Score 19.4; DB 1; Length 40;
 Best Local Similarity 70.3%; Pred. No. 1.5e+04;
 Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 132 CGTTGTACGCGCTTCCTGAGTAAGAAGAA 168
 Db 37 CGTTCTACCGCTTCAGTTCATTAGACGAGAACAA 1

RESULT 41

US-09-345-882-71
 : Sequence 71, Application US/09345882
 : Patent No. 6399373

GENERAL INFORMATION:
 : APPLICANT: Bougueleret, Lydie
 : TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)

FILE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.

FILE REFERENCE: GENSET.031A
 : CURRENT APPLICATION NUMBER: US/09/345.882
 : CURRENT FILING DATE: 1999-06-30
 : PRIOR APPLICATION NUMBER: US 60/091,315
 : PRIOR FILING DATE: 1998-06-30
 : PRIOR APPLICATION NUMBER: US 60/111,909
 : PRIOR FILING DATE: 1998-12-10
 : NUMBER OF SEQ ID NOS: 140
 : SOFTWARE: Patent.pm
 : SEQ ID NO 71
 : LENGTH: 47
 : TYPE: DNA

ORGANISM: Homo Sapiens
 : FEATURE:
 : NAME/KEY: allele
 : LOCATION: 1..47
 : OTHER INFORMATION: polymorphic fragment 99-1442-224, variant version of SEQ ID50
 : FEATURE:
 : NAME/KEY: allele
 : LOCATION: 24
 : OTHER INFORMATION: base T ; G in SEQ ID50
 : FEATURE:
 : NAME/KEY: primer_bind
 : LOCATION: 1..23
 : OTHER INFORMATION: potential microsequencing oligo 99-1442-224.mis1

FEATURE:
 : NAME/KEY: primer_bind
 : LOCATION: 25..47
 : OTHER INFORMATION: complement potential microsequencing oligo 99-1442-224.mis2
 : US-09-345-882-71

Query Match 0.8%; Score 19.4; DB 4; Length 47;
 Best Local Similarity 64.4%; Pred. No. 1.7e+04;
 Matches 29; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 2107 ATTATCCAGCCTATTGAGTAATAATTTGTTACTTTAGT 2151
 Db 1 ATTATCTCAGTCATATTGCGTTTCTTCTCTTAAT 45

RESULT 42
 : US-08-843-409-11/c
 : Sequence 11, Application US/08843409
 : Patent No. 6103235
 : GENERAL INFORMATION:

APPLICANT: Neville, David M.
 : APPLICANT: Sharif, Joshua E.
 : APPLICANT: Thompson, Jerry Todd
 : APPLICANT: Hu, Hualzhong
 : APPLICANT: Ma, Shenglin
 : TITLE OF INVENTION: AN IMMUNOTOXIN WITH IN VIVO T CELL
 : FILE REFERENCE: 14014.0205
 : CURRENT APPLICATION NUMBER: US/08/843.409
 : CURRENT FILING DATE: 1997-04-15
 : EARLIER APPLICATION NUMBER: 08/739,703
 : EARLIER FILING DATE: 1996-10-29
 : EARLIER APPLICATION NUMBER: 60/008,104
 : EARLIER FILING DATE: 1995-10-30
 : NUMBER OF SEQ ID NOS: 14
 : SOFTWARE: FastSeq for Windows Version 3.0
 : SEQ ID NO 11
 : LENGTH: 36
 : TYPE: DNA

ORGANISM: Artificial Sequence
 : FEATURE:
 : OTHER INFORMATION: oligonucleotide primer
 : OTHER INFORMATION: y is c or t
 : US-08-843-409-11

Query Match 0.8%; Score 19.2; DB 3; Length 36;
 Best Local Similarity 70.6%; Pred. No. 1.7e+04;

	Matches	24;	Conservative	1;	Mismatches	9;	Indels	0;	Gaps	0;						
QY	1865	TC	TG	GA	GC	CA	CT	CA	CA	GA	GC	CT	TG	GA	AG	1898
Db	36	TT	TG	GA	GC	CA	CT	CA	CA	GA	GC	CT	TG	GA	AG	3

RESULT 43
US-08-484

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1      Sequence 17, Application US/08484397A
2      Patent No. 5869055
3
4      GENERAL INFORMATION:
5
6      APPLICANT: Juan, Shao-Chieh
7      APPLICANT: Lichenstein, Henri S.
8      APPLICANT: Wright, Samuel D.
9      TITLE OF INVENTION: ANTI-INFLAMMATORY CD14 POLYPEPTIDES
10     NUMBER OF SPOUNCES: 38
11     CORRESPONDENCE ADDRESS:
12     ADDRESSEE: AMGEN INC
13     STREET: 1840 Dehavilland Drive
14     City: Thousand Oaks
15     STATE: CA
16     COUNTRY: US
17     ZIP: 91320-1789
18
19     COMPUTER READABLE FORM:
20     MEDIUM TYPE: Floppy disk
21     COMPUTER: IBM PC compatible
22     OPERATING SYSTEM: PC-DOS/MS-DOS
23     SOFTWARE: Patent In Release #1.0, Version #1.30
24
25     CURRENT APPLICATION DATA:
26     APPLICATION NUMBER: US/08/484,397A
27     FILING DATE: 07-JUN-1995
28     CLASSIFICATION: 424
29     ATTORNEY/AGENT INFORMATION:
30     NAME: Curry, Daniel R.
31     REGISTRATION NUMBER: 32,727
32     REFERENCE/DOCKET NUMBER: A-324A
33     TELECOMMUNICATION INFORMATION:
34     TELEPHONE: 805/447-1000
35     TELEFAX: 805/447-1090
36     INFORMATION FOR SEQ. ID NO: 17:
37     SEQUENCE CHARACTERISTICS:
38     LENGTH: 41 base pairs
39     TYPE: nucleic acid
40     STRANDEDNESS: single
41     TOPOLOGY: linear
42     MOLECULE TYPE: CDNA
43
44     US-08-484-397A-17

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Query Match	0.8%	Score 19.2	DB 2	Length 41
Best Local Similarity	67.5%	Pred No.1.8e+04		
Matches 27; Conservative		Mismatches 13;	Indels 0;	Gaps 0

RESULT 44
US-09-546-483-2/C
; Sequence 2, Application US/09546483

```

: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: Patentin Ver. 2.1
: SEQ ID NO 2
: LENGTH: 41
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: PCR PRIMER
: IS-03-346-483-2

```

QY	184 CATCAAGACCAACCAGGAGCAGGTGCCTACAT 215
Db	32 CTTCAAGACCATCTTGACTGAATTCATATAT 1

OTHER INFORMATION: Description of Artificial Sequence: PCR PRIMER
US-09-823-177-2

RESULT 46
 US-08-746-111-740/c
 : Sequence 40, Application US/08746111
 : Patent No. 6066778
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Ginsburg, David
 :
 : APPLICANT: Cui, Jisong
 :
 : TITLE OF INVENTION: Compositions And Methods For Screening
 : TITLE OF INVENTION: Compounds For Anticoagulant Activity
 :
 : NUMBER OF SEQUENCES: 54
 :
 : CORRESPONDENCE ADDRESS:
 :
 : ADDRESSEE: Medlen & Carroll, LLP
 :
 : STREET: 220 Montgomery Street, Suite 2200
 :
 : CITY: San Francisco
 :
 : STATE: California
 :
 : COUNTRY: United States of America
 :
 : ZIP: 94104
 :
 : COMPUTER READABLE FORM:
 :
 :

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/746,111
FILING DATE: 06-NOV-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-746-111-40

Query Match 0.8%; Score 19.2; DB 3; Length 42;
Best Local Similarity 67.5%; Pred. No. 1.8e+04;
Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY * 1446 TCATATGAGTGGAGAGAAAAGCTTATGATTCGATA 1485
DB 40 TCATAGAGACGAGAGAGAAAGGCTGAAAGCTCAGAGAAA 1

RESULT 47
US-09-284-832-29
Sequence 29, Application US/09284832
Patent No. 6287770
GENERAL INFORMATION:
APPLICANT: WESTON, Anthony
APPLICANT: ASSENBERG, Rene
APPLICANT: MARSH, Peter
APPLICANT: MOCK, Graham Andrew
APPLICANT: RAY, Trevor Duncan
APPLICANT: WHARAM, Susan Deborah
APPLICANT: CARDY, Donald Leonard Nicholas
TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO NUCLEIC ACID PROMOTERS
FILE REFERENCE: 41301/258923
CURRENT APPLICATION NUMBER: US/09/284,832
CURRENT FILING DATE: 1998-04-16
EARLIER FILING DATE: 1998-01-27
EARLIER FILING DATE: 1998-01-27
EARLIER FILING DATE: 1998-01-27
EARLIER FILING DATE: 1998-07-08
EARLIER FILING DATE: 1998-07-08
EARLIER FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 29
LENGTH: 45
TYPE: DNA
ORGANISM: CFTR CS Probe with SP6 Promoter
US-09-284-832-29

Query Match 0.8%; Score 19.2; DB 4; Length 45;
Best Local Similarity 67.5%; Pred. No. 1.9e+04;
Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 250 ATGCATCATATATAACACAGAACTTGATTAAGTGACA 289
DB 1 ATTCATCATAGGAACACCAAGATGATATTAGGTGACA 40

RESULT 48

US-09-641-638-931/c
Sequence 931, Application US/09641638
Patent No. 6432648
GENERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Bouguetel, Lydie
APPLICANT: Chumakov, Ilya
APPLICANT: Cohen, Annick
TITLE OF INVENTION: BIALLIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
FILE REFERENCE: GENSET.051Cp1
CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
SOFTWARE: Patent. pm
SEQ ID NO 931
LENGTH: 47
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 12-834-183 : polymorphic base A or G
US-09-641-638-931

Query Match 0.8%; Score 19.2; DB 4; Length 47;
Best Local Similarity 70.6%; Pred. No. 2e+04;
Matches 24; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1134 TTTTATATATGTTATTCATTTGTCAGCTGTCTAA 1167
DB 35 TTTGTTTACAYTGTTTCATTTGTTGACTGAGAAA 2

RESULT 49
US-08-471-791-35/c
Sequence 35, Application US/08471791
Patent No. 5723595
GENERAL INFORMATION:
APPLICANT: Thompson, Gregory A
APPLICANT: Knaut, Vic C
TITLE OF INVENTION: Plant Desaturases-Compositions
TITLE OF INVENTION: and Uses
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: California
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1 (a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,791
FILING DATE: 6-JUNE-95
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/762,762
FILING DATE: 16-SEPT-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US91/01746
FILING DATE: 14-MAR-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/615,784
FILING DATE: 14-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/567,373
FILING DATE: 13-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/494,106
FILING DATE: 16-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Lassen, Elizabeth
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 69-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
TELEX: 350370 CGNE
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: synthetic oligonucleotide
US-08-471-791-35

Query Match 0.8%; Score 19.2; DB 1; Length 48;
Best Local Similarity 67.5%; Pred. No. 2e+04;
Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 155 AAGAGAAGAAAATGTACCATGCATCCATCAAGACCA 194
|||||
Db 47 AAGAGAAGAAAATGTACCATGCATCCATCAAGACCA 194

RESULT 50

PCT-US91-01746-35/C

Sequence 35, Application PC/TUS9101746

GENERAL INFORMATION:

APPLICANT: Thompson, Gregory A

APPLICANT: Knaut, Vic C

TITLE OF INVENTION: Plant Desaturases-Compositions and Uses

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: Calgene, Inc.

STREET: 1920 Fifth Street

CITY: Davis

STATE: California

COUNTRY: USA

ZIP: 95616

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB storage

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 6.0.7

SOFTWARE: Microsoft Word 4.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US91/01746

FILING DATE: 19910314

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/615,784

FILING DATE: 14-NOV-1990

APPLICATION NUMBER: 07/567,373

FILING DATE: 13-AUG-1990

APPLICATION NUMBER: 07/494,106

FILING DATE: 16-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Lassen, Elizabeth
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
REFERENCE/DOCKET NUMBER: CGNE 69-3 WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
TELEX: 350370 CGNE
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: synthetic oligonucleotide
PCT-US91-01746-35

Query Match 0.8%; Score 19.2; DB 5; Length 48;
Best Local Similarity 67.5%; Pred. No. 2e+04;
Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 155 AAGAGAAGAAAATGTACCATGCATCCATCAAGACCA 194
|||||
Db 47 AAGAGAAGAAAATGTACCATGCATCCATCAAGACCA 194

Search completed: November 11, 2002, 02:36:25
Job time: 117 secs

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OM nucleic - nucleic search, using sw model

Run on: November 11, 2002, 00:01:12 ; Search time 131 Seconds
(without alignments)
6253.432 Million cell updates/sec

Title: US-09-659-860A-3
Perfect score: 2309
Sequence: 1 gagagacgtgtgcacatccca.....gattaaatgtgtgtt 2309

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 320260 seqs, 17792727 residues

Total number of hits satisfying chosen parameters: 164392

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1000 summaries

Database :

Published Applications_NA: *
1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq: *
2: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq: *
3: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq: *
4: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq: *
5: /cgn2_6/prodata/1/pubpna/PCTUS_PUBCOMB.seq: *
6: /cgn2_6/prodata/1/pubpna/US08_NEW_PUB.seq: *
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9: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq: *
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11: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq: *
12: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq: *
13: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq: *
14: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22.8	1.0	49	12	US-10-108-280-6
2	21.8	0.9	49	10	US-09-975-408-59
3	21.8	0.9	49	12	US-10-075-579-59
4	21.4	0.9	45	10	US-09-820-171-27
5	21.2	0.9	48	10	US-09-790-417-150
6	21.0	0.9	21	10	US-09-944-851-7
7	20.6	0.9	41	12	US-10-108-280-21
8	20.6	0.9	45	12	US-10-108-280-5
9	20.0	0.9	44	10	US-09-839-743-28
10	19.8	0.9	47	10	US-09-756-095-32
11	19.4	0.8	21	10	US-09-944-851-9
12	19.4	0.8	43	10	US-09-774-021-17
13	19.2	0.8	40	10	US-09-809-905-4
14	19.0	0.8	19	10	US-09-944-851-5
15	19.0	0.8	46	10	US-09-884-260A-48
16	18.6	0.8	36	9	US-09-284-249-2
17	18.6	0.8	39	10	US-09-867-262-13
18	18.6	0.8	39	10	US-09-885-551A-13
19	18.6	0.8	39	12	US-10-087-426-13

20	18.6	0.8	41	12	US-10-108-280-4	Sequence 4, Appl
21	18.6	0.8	42	10	US-09-997-956-3	Sequence 1, Appl
22	18.4	0.8	46	9	US-09-771-372-1	Sequence 1, Appl
23	18.4	0.8	50	9	US-09-440-829-14	Sequence 14, Appl
24	18.2	0.8	50	10	US-09-734-836-5	Sequence 5, Appl
25	18.0	0.8	18	10	US-09-944-851-8	Sequence 8, Appl
26	18.0	0.8	18	10	US-09-944-851-11	Sequence 11, Appl
27	18.0	0.8	21	10	US-09-944-851-10	Sequence 10, Appl
28	18.0	0.8	37	10	US-09-263-959-743	Sequence 743, App
29	18.0	0.8	37	10	US-09-263-959-801	Sequence 801, App
30	17.8	0.8	31	10	US-09-784-990-33	Sequence 33, Appl
31	17.8	0.8	36	10	US-09-839-743-1	Sequence 1, Appl
32	17.8	0.8	37	12	US-10-081-281-11	Sequence 11, Appl
33	17.8	0.8	45	10	US-09-962-055-30	Sequence 30, Appl
34	17.8	0.8	45	12	US-10-023-529-30	Sequence 30, Appl
35	17.8	0.8	45	12	US-10-023-523-30	Sequence 30, Appl
36	17.8	0.8	48	9	US-09-956-086-32	Sequence 32, Appl
37	17.8	0.8	48	9	US-09-956-087-32	Sequence 32, Appl
38	17.8	0.8	50	9	US-09-440-829-26	Sequence 26, Appl
39	17.6	0.8	28	10	US-09-334-923A-49	Sequence 49, Appl
40	17.6	0.8	28	10	US-09-334-954A-49	Sequence 49, Appl
41	17.6	0.8	36	9	US-09-985-442-13	Sequence 13, Appl
42	17.6	0.8	36	10	US-09-935-727-40	Sequence 40, Appl
43	17.6	0.8	36	10	US-09-983-580-13	Sequence 13, Appl
44	17.6	0.8	40	10	US-09-834-291-18	Sequence 18, Appl
45	17.6	0.8	40	10	US-09-834-291-26	Sequence 26, Appl
46	17.6	0.8	41	10	US-09-238-351-29	Sequence 29, Appl
47	17.6	0.8	42	10	US-09-737-626A-3	Sequence 3, Appl
48	17.6	0.8	45	9	US-10-104-611-18	Sequence 18, Appl
49	17.6	0.8	45	9	US-10-112-547-18	Sequence 18, Appl
50	17.6	0.8	45	10	US-09-965-602-27	Sequence 27, Appl
51	17.6	0.8	45	10	US-09-872-349-32	Sequence 32, Appl
52	17.6	0.8	48	10	US-09-056-160B-44	Sequence 44, Appl
53	17.6	0.8	48	9	US-09-858-200A-1	Sequence 1, Appl
54	17.4	0.8	39	9	US-09-252-150-59	Sequence 59, Appl
55	17.4	0.8	42	10	US-09-749-234A-14	Sequence 14, Appl
56	17.4	0.8	44	10	US-09-988-899-56	Sequence 56, Appl
57	17.4	0.8	44	10	US-09-900-062-24	Sequence 24, Appl
58	17.4	0.8	47	9	US-09-935-371-51	Sequence 51, Appl
59	17.4	0.8	47	10	US-09-374-671-98	Sequence 98, Appl
60	17.4	0.8	50	9	US-09-992-598-163	Sequence 163, App
61	17.4	0.8	50	10	US-09-504-221A-3057	Sequence 3057, Ap
62	17.4	0.8	50	10	US-09-810-936-269	Sequence 269, App
63	17.4	0.8	50	10	US-09-989-722-163	Sequence 163, App
64	17.4	0.8	50	10	US-09-989-723-163	Sequence 163, App
65	17.4	0.8	50	10	US-09-989-279-163	Sequence 163, App
66	17.4	0.8	50	10	US-09-989-727-163	Sequence 163, App
67	17.4	0.8	50	10	US-09-274-553D-3057	Sequence 3057, Ap
68	17.4	0.8	50	10	US-09-989-731-163	Sequence 163, App
69	17.4	0.8	50	10	US-09-429-755-269	Sequence 269, App
70	17.4	0.8	50	10	US-09-989-732-163	Sequence 163, App
71	17.4	0.8	50	10	US-09-991-073-163	Sequence 163, App
72	17.4	0.8	50	10	US-09-990-442-163	Sequence 163, App
73	17.4	0.8	50	10	US-09-991-163-163	Sequence 163, App
74	17.4	0.8	50	10	US-09-993-604-163	Sequence 163, App
75	17.4	0.8	50	10	US-09-990-456-163	Sequence 163, App
76	17.4	0.8	50	10	US-09-989-721-163	Sequence 163, App
77	17.4	0.8	50	10	US-09-297-910-13	Sequence 13, Appl
78	17.4	0.8	50	10	US-09-297-910-14	Sequence 14, Appl
79	17.2	0.7	30	10	US-09-371-307-81	Sequence 81, Appl
80	17.2	0.7	34	10	US-09-971-187-6	Sequence 6, Appl
81	17.2	0.7	35	12	US-09-952-385-4	Sequence 4, Appl
82	17.2	0.7	35	12	US-10-000-759A-4	Sequence 4, Appl
83	17.2	0.7	37	10	US-09-758-317-1	Sequence 1, Appl
84	17.2	0.7	40	9	US-09-863-040-25	Sequence 25, Appl
85	17.2	0.7	40	9	US-09-863-040-26	Sequence 26, Appl
86	17.2	0.7	40	10	US-09-238-351-73	Sequence 73, Appl
87	17.2	0.7	41	10	US-09-238-351-40	Sequence 40, Appl
88	17.2	0.7	44	10	US-09-803-165-2	Sequence 2, Appl
89	17.2	0.7	50	10	US-09-504-231A-3036	Sequence 3036, Ap
90	17.2	0.7	50	10	US-09-274-553D-3036	Sequence 3036, Ap
91	17.2	0.7	50	10	US-09-274-553D-3086	Sequence 3086, Ap
92	17.2	0.7	50	10	US-09-274-553D-3086	Sequence 3086, Ap

93	17	0.7	20	10	US-09-825-922-5	Sequence 5, Appli	166	16.2	0.7	30	9	US-09-982-107-15	Sequence 16, Appl
C 94	17	0.7	30	9	US-09-840-243B-8	Sequence 8, Appli	C 167	16.2	0.7	30	10	US-09-760-574-99	Sequence 99, Appl
95	17	0.7	30	10	US-09-272-162-7	Sequence 7, Appli	C 168	16.2	0.7	30	10	US-09-765-272-117	Sequence 417, Appl
96	17	0.7	35	8	US-09-973-028-9	Sequence 9, Appli	169	16.2	0.7	30	10	US-09-333-527-18	Sequence 18, Appl
97	17	0.7	36	9	US-09-985-442-12	Sequence 12, Appl	170	16.2	0.7	31	10	US-09-801-274-81	Sequence 81, Appl
98	17	0.7	36	10	US-09-848-164-114	Sequence 14, Appl	C 171	16.2	0.7	31	10	US-09-801-274-81	Sequence 94, Appl
99	17	0.7	36	10	US-09-983-580-12	Sequence 12, Appl	172	16.2	0.7	31	10	US-09-263-059-880	Sequence 560, Appl
100	17	0.7	43	10	US-09-993-170-21	Sequence 21, Appl	173	16.2	0.7	32	10	US-09-982-308-20	Sequence 20, Appl
C 101	17	0.7	44	10	US-09-983-170-21	Sequence 21, Appl	174	16.2	0.7	38	10	US-09-784-990-24	Sequence 24, Appl
C 102	17	0.7	45	10	US-09-983-165-4	Sequence 4, Appli	175	16.2	0.7	38	10	US-09-874-547-84	Sequence 84, Appl
103	17	0.7	45	10	US-09-918-889-28	Sequence 28, Appl	176	16.2	0.7	40	9	US-10-007-448-4	Sequence 4, Appli
104	17	0.7	45	10	US-09-919-942-28	Sequence 28, Appl	C 177	16.2	0.7	40	9	US-09-863-040-25	Sequence 25, Appl
105	17	0.7	45	10	US-09-765-272-235	Sequence 235, Appl	C 178	16.2	0.7	40	9	US-09-863-040-25	Sequence 26, Appl
C 106	17	0.7	50	10	US-09-504-231A-2975	Sequence 2975, Appl	179	16.2	0.7	40	10	US-09-728-847-31	Sequence 31, Appl
C 107	17	0.7	50	10	US-09-274-553D-3048	Sequence 3048, Ap	C 180	16.2	0.7	40	10	US-09-027-287-11	Sequence 11, Appl
C 108	16.8	0.7	31	10	US-09-808-212A-28	Sequence 28, Appl	C 181	16.2	0.7	40	10	US-09-027-287-11	Sequence 15, Appl
109	16.8	0.7	31	10	US-09-801-274-72	Sequence 27, Appl	C 182	16.2	0.7	40	10	US-09-252-656B-11	Sequence 11, Appl
110	16.8	0.7	33	10	US-09-976-178-10	Sequence 10, Appl	C 183	16.2	0.7	43	9	US-10-081-408-7	Sequence 7, Appli
111	16.8	0.7	33	10	US-09-911-253-10	Sequence 10, Appl	C 184	16.2	0.7	44	10	US-09-803-165-3	Sequence 3, Appli
112	16.8	0.7	33	10	US-09-971-611-21	Sequence 21, Appl	C 185	16.2	0.7	44	10	US-09-803-165-3	Sequence 5, Appli
113	16.8	0.7	37	12	US-09-883-489-4	Sequence 4, Appli	C 186	16.2	0.7	44	10	US-09-803-165-3	Sequence 7, Appli
114	16.8	0.7	37	12	US-10-108-280-3	Sequence 3, Appli	C 187	16.2	0.7	44	10	US-09-803-165-3	Sequence 7, Appli
C 115	16.8	0.7	39	10	US-09-774-414-30	Sequence 30, Appl	C 188	16.2	0.7	44	10	US-09-803-165-3	Sequence 7, Appli
C 116	16.8	0.7	41	10	US-09-782-361-18	Sequence 18, Appl	C 189	16.2	0.7	46	10	US-09-835-147-22	Sequence 22, Appl
C 117	16.8	0.7	42	9	US-09-996-140-29	Sequence 29, Appl	C 190	16.2	0.7	47	10	US-09-816-825-8	Sequence 8, Appli
C 118	16.8	0.7	42	10	US-09-764-304-13	Sequence 13, Appl	C 191	16.2	0.7	47	10	US-09-816-825-8	Sequence 8, Appli
119	16.8	0.7	48	10	US-09-756-551A-14	Sequence 14, Appl	C 192	16.2	0.7	47	10	US-09-808-599-20	Sequence 20, Appl
C 120	16.8	0.7	50	9	US-09-440-829-32	Sequence 32, Appl	C 193	16.2	0.7	47	10	US-09-908-599-20	Sequence 22, Appl
C 121	16.6	0.7	34	10	US-09-932-678-6	Sequence 6, Appli	C 194	16.2	0.7	47	10	US-09-901-884A-210	Sequence 210, Appl
C 122	16.6	0.7	36	10	US-09-839-743-1	Sequence 1, Appli	C 195	16.2	0.7	48	10	US-09-978-273-7	Sequence 7, Appli
123	16.6	0.7	40	10	US-09-951-401-25	Sequence 25, Appl	196	16.2	0.7	48	10	US-09-978-273-7	Sequence 56, Appl
124	16.6	0.7	40	10	US-09-922-101-25	Sequence 25, Appl	197	16.2	0.7	48	10	US-09-931-087A-33	Sequence 33, Appl
125	16.6	0.7	42	10	US-09-755-633-2	Sequence 32, Appli	C 198	16.2	0.7	50	10	US-09-909-496-2	Sequence 2, Appli
C 126	16.6	0.7	46	9	US-09-905-291A-32	Sequence 32, Appl	C 199	16.2	0.7	50	10	US-09-909-496-2	Sequence 2, Appli
C 127	16.6	0.7	46	10	US-09-909-920-32	Sequence 32, Appl	C 200	16.2	0.7	50	10	US-09-909-496-2	Sequence 2, Appli
C 128	16.6	0.7	47	10	US-09-909-920-32	Sequence 32, Appl	C 201	16.2	0.7	50	10	US-09-911-047-2	Sequence 2, Appli
C 129	16.6	0.7	50	9	US-09-901-884A-324	Sequence 324, App	C 202	16.2	0.7	50	12	US-10-120-092-2	Sequence 2, Appli
C 130	16.6	0.7	50	9	US-09-978-295A-167	Sequence 167, App	C 203	16.2	0.7	50	12	US-10-120-092-2	Sequence 3, Appli
C 131	16.4	0.7	20	10	US-09-263-959-459	Sequence 459, App	C 204	16	0.7	25	10	US-09-866-108-13693	Sequence 13693, A
132	16.4	0.7	31	10	US-09-907-574-1	Sequence 1, Appli	C 205	16	0.7	25	10	US-09-866-108-13694	Sequence 13694, A
133	16.4	0.7	31	10	US-09-068-528B-1	Sequence 8, Appli	C 206	16	0.7	25	10	US-09-866-108-13694	Sequence 15406, A
134	16.4	0.7	33	9	US-10-008-620-8	Sequence 26, Appl	C 207	16	0.7	25	10	US-09-866-108-13694	Sequence 15406, A
135	16.4	0.7	33	9	US-09-840-037A-26	Sequence 26, Appl	C 208	16	0.7	25	10	US-09-866-108-13694	Sequence 558, App
C 136	16.4	0.7	35	10	US-09-895-211-9	Sequence 9, Appli	C 209	16	0.7	31	10	US-09-801-274-558	Sequence 558, App
C 137	16.4	0.7	36	10	US-10-127-733-5	Sequence 5, Appli	C 210	16	0.7	31	10	US-09-801-274-558	Sequence 567, App
C 138	16.4	0.7	36	12	US-08-424-550B-623	Sequence 623, App	C 211	16	0.7	31	10	US-09-801-274-558	Sequence 823, App
C 139	16.4	0.7	38	8	US-09-903-456-112	Sequence 12, Appl	C 212	16	0.7	33	10	US-09-822-261-102	Sequence 102, App
C 140	16.4	0.7	39	10	US-09-264-468B-12	Sequence 37, Appl	C 213	16	0.7	33	9	US-09-771-009-67	Sequence 67, Appl
C 141	16.4	0.7	40	10	US-09-371-307-37	Sequence 21, Appl	C 214	16	0.7	35	10	US-09-426-548-34	Sequence 34, Appl
142	16.4	0.7	41	10	US-09-980-046-21	Sequence 14, Appl	C 215	16	0.7	35	10	US-09-732-561-12	Sequence 92, Appl
143	16.4	0.7	45	9	US-09-827-289-14	Sequence 18, Appl	C 216	16	0.7	36	10	US-09-848-164-92	Sequence 92, Appl
144	16.4	0.7	45	10	US-09-827-289-14	Sequence 18, Appl	C 217	16	0.7	37	10	US-09-765-272-340	Sequence 340, Appl
145	16.4	0.7	45	10	US-09-777-430A-24	Sequence 29, Appl	C 218	16	0.7	38	10	US-09-774-414-31	Sequence 31, Appl
C 146	16.4	0.7	45	10	US-09-795-006A-38	Sequence 66, Appl	C 219	16	0.7	39	10	US-09-865-579A-27	Sequence 27, Appl
C 147	16.4	0.7	46	10	US-09-918-601-66	Sequence 101, Appl	C 220	16	0.7	39	10	US-09-921-942B-3	Sequence 3, Appli
C 148	16.4	0.7	46	10	US-09-918-601-66	Sequence 66, Appl	C 221	16	0.7	40	10	US-09-738-847-27	Sequence 27, Appl
149	16.4	0.7	47	10	US-09-931-087A-9	Sequence 101, App	C 222	16	0.7	40	10	US-09-955-980-9	Sequence 12, Appl
150	16.4	0.7	48	10	US-09-931-087A-35	Sequence 35, Appl	C 223	16	0.7	41	10	US-09-955-980-9	Sequence 42, Appl
151	16.4	0.7	48	10	US-09-931-087A-35	Sequence 35, Appl	C 224	16	0.7	41	10	US-09-931-087A-35	Sequence 42, Appl
152	16.4	0.7	48	10	US-09-931-087A-35	Sequence 35, Appl	C 225	16	0.7	42	9	US-09-942-087A-32	Sequence 32, Appl
153	16.4	0.7	48	10	US-09-931-087A-35	Sequence 35, Appl	C 226	16	0.7	42	9	US-09-942-087A-32	Sequence 428, App
C 154	16.4	0.7	49	10	US-09-931-087A-35	Sequence 35, Appl	C 227	16	0.7	43	10	US-09-765-272-428	Sequence 24, Appl
C 155	16.4	0.7	50	9	US-09-931-087A-35	Sequence 35, Appl	C 228	16	0.7	44	10	US-09-765-272-428	Sequence 24, Appl
156	16.4	0.7	50	10	US-09-504-231A-2947	Sequence 2947, Ap	C 229	16	0.7	45	10	US-09-765-272-428	Sequence 320, App
157	16.4	0.7	50	10	US-09-504-231A-2947	Sequence 2947, Ap	C 230	16	0.7	45	10	US-09-765-272-428	Sequence 320, App
158	16.4	0.7	50	10	US-09-504-231A-2947	Sequence 2947, Ap	C 231	16	0.7	45	10	US-09-765-272-428	Sequence 320, App
159	16.4	0.7	50	10	US-09-504-231A-2947	Sequence 2947, Ap	C 232	16	0.7	46	10	US-09-765-272-428	Sequence 320, App
160	16.4	0.7	50	10	US-09-274-553D-2961	Sequence 2961, Ap	C 233	16	0.7	46	10	US-09-765-272-428	Sequence 320, App
161	16.4	0.7	50	10	US-09-274-553D-2961	Sequence 2961, Ap	C 234	16	0.7	47	8	US-08-973-391A-2	Sequence 2, Appli
162	16.4	0.7	50	10	US-09-274-553D-2961	Sequence 2961, Ap	C 235	16	0.7	48	10	US-09-922-261-233	Sequence 233, App
163	16.4	0.7	50	10	US-09-274-553D-2961	Sequence 2961, Ap	C 236	16	0.7	48	10	US-09-922-261-233	Sequence 233, App
C 164	16.2	0.7	27	10	US-10-036-342-33	Sequence 33, Appl	C 237	16	0.7	48	12	US-09-822-698A-48	Sequence 48, Appl
C 165	16.2	0.7	27	10	US-09-790-417-99	Sequence 99, Appl	C 238	16	0.7	49	9	US-10-026-385-8	Sequence 8, Appli
			27	10	US-09-954-764-2	Sequence 2, Appli				49	10	US-09-858-200A-2	Sequence 2, Appli
										49	10	US-09-738-847-16	Sequence 16, Appl

239	16	0.7	49	10	US-09-943-215-4	Sequence 4, Appl1	c 312	15.8	0.7	50	10	US-09-274-553D-2973	Sequence 2973, Ap
240	16	0.7	50	10	US-09-740-002-7	Sequence 7, Appl1	c 313	15.8	0.7	50	10	US-09-274-553D-2994	Sequence 2994, Ap
241	16	0.7	50	10	US-09-504-231A-2910	Sequence 2910, Ap	c 314	15.8	0.7	50	10	US-09-274-553D-3028	Sequence 3028, Ap
242	16	0.7	50	10	US-09-504-231A-2932	Sequence 2932, Ap	c 315	15.6	0.7	24	10	US-09-909-446-7	Sequence 7, Appl1
243	16	0.7	50	10	US-09-504-231A-3052	Sequence 3052, Ap	c 316	15.6	0.7	24	10	US-09-909-446-11	Sequence 11, Appl1
244	16	0.7	50	10	US-09-504-231A-3071	Sequence 3071, Ap	c 317	15.6	0.7	24	10	US-09-909-325-7	Sequence 7, Appl1
245	16	0.7	50	10	US-09-504-231A-3085	Sequence 3085, Ap	c 318	15.6	0.7	24	10	US-09-909-325-11	Sequence 11, Appl1
246	16	0.7	50	10	US-09-274-553D-2910	Sequence 2910, Ap	c 319	15.6	0.7	24	10	US-09-909-326-7	Sequence 7, Appl1
247	16	0.7	50	10	US-09-274-553D-2932	Sequence 2932, Ap	c 320	15.6	0.7	24	10	US-09-909-326-11	Sequence 11, Appl1
248	16	0.7	50	10	US-09-274-553D-3052	Sequence 3052, Ap	c 321	15.6	0.7	27	10	US-09-978-730-9	Sequence 9, Appl1
249	16	0.7	50	10	US-09-274-553D-3071	Sequence 3071, Ap	c 322	15.6	0.7	29	9	US-09-863-040-51	Sequence 51, Appl1
250	16	0.7	50	10	US-09-274-553D-3085	Sequence 3085, Ap	c 323	15.6	0.7	30	10	US-09-788-657-1	Sequence 1, Appl1
251	15.8	0.7	22	10	US-09-895-652-30	Sequence 30, Appl1	c 324	15.6	0.7	31	10	US-09-801-274-1579	Sequence 1579, Ap
252	15.8	0.7	27	10	US-09-749-601A-7	Sequence 7, Appl1	c 325	15.6	0.7	32	10	US-09-345-790-9	Sequence 9, Appl1
253	15.8	0.7	27	10	US-09-860-793-24	Sequence 24, Appl1	c 326	15.6	0.7	35	10	US-09-179-536B-137	Sequence 137, App
254	15.8	0.7	31	10	US-09-801-274-178	Sequence 178, App	c 327	15.6	0.7	35	10	US-09-946-334-5	Sequence 5, Appl1
255	15.8	0.7	31	10	US-09-801-274-1508	Sequence 1508, Ap	c 328	15.6	0.7	35	10	US-09-946-334-6	Sequence 6, Appl1
256	15.8	0.7	31	10	US-09-801-274-1784	Sequence 1784, Ap	c 329	15.6	0.7	35	10	US-09-386-380-7	Sequence 7, Appl1
257	15.8	0.7	34	10	US-09-923-246-57	Sequence 57, Appl1	c 330	15.6	0.7	36	10	US-09-386-380-11	Sequence 11, Appl1
258	15.8	0.7	35	10	US-09-728-466-22	Sequence 22, Appl1	c 331	15.6	0.7	37	10	US-09-854-799-15	Sequence 15, Appl1
259	15.8	0.7	35	10	US-09-728-466-23	Sequence 23, Appl1	c 332	15.6	0.7	38	10	US-09-929-493-31	Sequence 31, Appl1
260	15.8	0.7	35	10	US-09-915-060-12	Sequence 12, Appl1	c 333	15.6	0.7	39	10	US-09-804-661-18	Sequence 18, Appl1
261	15.8	0.7	35	12	US-10-109-886-2	Sequence 2, Appl1	c 334	15.6	0.7	42	10	US-09-286-240-15	Sequence 15, Appl1
262	15.8	0.7	36	10	US-09-426-548-155	Sequence 155, App	c 335	15.6	0.7	42	10	US-09-951-401-18	Sequence 18, Appl1
263	15.8	0.7	36	10	US-09-848-164-26	Sequence 26, Appl1	c 336	15.6	0.7	42	10	US-09-922-101-34	Sequence 34, Appl1
264	15.8	0.7	36	10	US-09-766-378A-6	Sequence 6, Appl1	c 337	15.6	0.7	43	10	US-09-738-396-35	Sequence 35, Appl1
265	15.8	0.7	38	8	US-08-961-888-38	Sequence 38, Appl1	c 338	15.6	0.7	43	10	US-09-738-396-35	Sequence 35, Appl1
266	15.8	0.7	38	10	US-09-738-968-33	Sequence 33, Appl1	c 339	15.6	0.7	43	10	US-09-887-469-23	Sequence 23, Appl1
267	15.8	0.7	39	10	US-09-765-272-286	Sequence 286, App	c 340	15.6	0.7	44	9	US-09-910-518A-5	Sequence 5, Appl1
268	15.8	0.7	40	10	US-09-245-802-18	Sequence 18, Appl1	c 341	15.6	0.7	44	9	US-09-978-295A-43	Sequence 43, Appl1
269	15.8	0.7	40	10	US-09-848-164-39	Sequence 39, Appl1	c 342	15.6	0.7	44	10	US-09-839-743-28	Sequence 28, Appl1
270	15.8	0.7	41	9	US-10-003-035-62	Sequence 62, Appl1	c 343	15.6	0.7	45	9	US-09-939-483-24	Sequence 24, Appl1
271	15.8	0.7	41	10	US-09-951-401-45	Sequence 45, Appl1	c 344	15.6	0.7	45	10	US-09-905-291A-146	Sequence 146, App
272	15.8	0.7	41	10	US-09-922-101-45	Sequence 45, Appl1	c 345	15.6	0.7	45	10	US-09-838-386-13	Sequence 13, Appl1
273	15.8	0.7	42	10	US-09-349-954A-12	Sequence 12, Appl1	c 346	15.6	0.7	45	10	US-09-909-320-146	Sequence 146, App
274	15.8	0.7	42	10	US-09-907-007-12	Sequence 12, Appl1	c 347	15.6	0.7	46	10	US-09-835-147-22	Sequence 22, Appl1
275	15.8	0.7	44	10	US-09-899-980A-27	Sequence 27, Appl1	c 348	15.6	0.7	46	10	US-09-932-679-22	Sequence 22, Appl1
276	15.8	0.7	45	10	US-09-989-962-17	Sequence 17, Appl1	c 349	15.6	0.7	46	10	US-10-003-035-67	Sequence 67, Appl1
277	15.8	0.7	45	10	US-09-781-901-11	Sequence 11, Appl1	c 350	15.6	0.7	47	9	US-10-003-035-68	Sequence 68, Appl1
278	15.8	0.7	46	10	US-09-369-735B-4	Sequence 4, Appl1	c 351	15.6	0.7	47	10	US-09-909-496-9	Sequence 9, Appl1
279	15.8	0.7	46	10	US-09-906-397-6	Sequence 6, Appl1	c 352	15.6	0.7	47	10	US-09-987-456-26	Sequence 26, Appl1
280	15.8	0.7	46	10	US-09-906-397-7	Sequence 7, Appl1	c 353	15.6	0.7	47	10	US-09-939-484-24	Sequence 24, Appl1
281	15.8	0.7	47	10	US-09-765-272-391	Sequence 391, App	c 354	15.6	0.7	48	10	US-09-217-268B-16	Sequence 16, Appl1
282	15.8	0.7	47	10	US-09-901-484A-198	Sequence 198, App	c 355	15.6	0.7	48	10	US-09-504-231A-2969	Sequence 2969, Ap
283	15.8	0.7	47	10	US-09-901-484A-229	Sequence 229, App	c 356	15.6	0.7	48	10	US-09-939-483-24	Sequence 24, Appl1
284	15.8	0.7	47	10	US-09-901-484A-240	Sequence 240, App	c 357	15.6	0.7	48	10	US-09-931-087A-34	Sequence 34, Appl1
285	15.8	0.7	47	10	US-09-901-484A-329	Sequence 329, App	c 358	15.6	0.7	49	10	US-09-790-417-117	Sequence 117, App
286	15.8	0.7	48	9	US-09-760-500A-32	Sequence 32, Appl1	c 359	15.6	0.7	49	10	US-09-790-417-118	Sequence 118, App
287	15.8	0.7	48	9	US-09-760-500A-64	Sequence 64, Appl1	c 360	15.6	0.7	50	10	US-09-504-231A-2940	Sequence 2940, Ap
288	15.8	0.7	48	9	US-09-918-543-18	Sequence 18, Appl1	c 361	15.6	0.7	50	10	US-09-504-231A-2956	Sequence 2956, Ap
289	15.8	0.7	48	9	US-09-967-409A-32	Sequence 32, Appl1	c 362	15.6	0.7	50	10	US-09-504-231A-2969	Sequence 2969, Ap
290	15.8	0.7	48	9	US-09-967-409A-64	Sequence 64, Appl1	c 363	15.6	0.7	50	10	US-09-504-231A-2981	Sequence 2981, Ap
291	15.8	0.7	48	9	US-09-975-062A-32	Sequence 32, Appl1	c 364	15.6	0.7	50	10	US-09-504-231A-3009	Sequence 3009, Ap
292	15.8	0.7	48	9	US-09-975-062A-64	Sequence 64, Appl1	c 365	15.6	0.7	50	10	US-09-504-231A-3047	Sequence 3047, Ap
293	15.8	0.7	48	9	US-09-976-378A-32	Sequence 32, Appl1	c 366	15.6	0.7	50	10	US-09-504-231A-3051	Sequence 3051, Ap
294	15.8	0.7	48	9	US-09-976-378A-64	Sequence 64, Appl1	c 367	15.6	0.7	50	10	US-09-504-231A-3094	Sequence 3094, Ap
295	15.8	0.7	48	9	US-09-976-577-32	Sequence 32, Appl1	c 368	15.6	0.7	50	10	US-09-504-231A-3094	Sequence 3094, Ap
296	15.8	0.7	48	9	US-09-976-577-64	Sequence 64, Appl1	c 369	15.6	0.7	50	10	US-09-274-553D-2940	Sequence 2940, Ap
297	15.8	0.7	48	10	US-09-973-788A-32	Sequence 32, Appl1	c 370	15.6	0.7	50	10	US-09-274-553D-2956	Sequence 2956, Ap
298	15.8	0.7	48	10	US-09-973-788A-64	Sequence 64, Appl1	c 371	15.6	0.7	50	10	US-09-274-553D-2969	Sequence 2969, Ap
299	15.8	0.7	48	10	US-09-923-625-32	Sequence 32, Appl1	c 372	15.6	0.7	50	10	US-09-274-553D-2981	Sequence 2981, Ap
300	15.8	0.7	48	10	US-09-973-638A-32	Sequence 32, Appl1	c 373	15.6	0.7	50	10	US-09-274-553D-3009	Sequence 3009, Ap
301	15.8	0.7	48	10	US-09-973-638A-64	Sequence 64, Appl1	c 374	15.6	0.7	50	10	US-09-274-553D-3047	Sequence 3047, Ap
302	15.8	0.7	48	10	US-09-974-007-32	Sequence 32, Appl1	c 375	15.6	0.7	50	10	US-09-274-553D-3051	Sequence 3051, Ap
303	15.8	0.7	48	10	US-09-974-007-64	Sequence 64, Appl1	c 376	15.6	0.7	50	10	US-09-274-553D-3094	Sequence 3094, Ap
304	15.8	0.7	48	10	US-09-976-617A-32	Sequence 32, Appl1	c 377	15.6	0.7	50	10	US-09-274-553D-3065	Sequence 3065, Ap
305	15.8	0.7	48	10	US-09-976-617A-64	Sequence 64, Appl1	c 378	15.6	0.7	50	10	US-09-274-553D-3094	Sequence 3094, Ap
306	15.8	0.7	48	10	US-09-961-949A-32	Sequence 32, Appl1	c 379	15.6	0.7	50	10	US-09-853-798-6	Sequence 6, Appl1
307	15.8	0.7	48	10	US-09-961-949A-64	Sequence 64, Appl1	c 380	15.6	0.7	50	10	US-09-783-590-6670	Sequence 6670, Ap
308	15.8	0.7	50	9	US-09-978-295A-83	Sequence 83, Appl1	c 381	15.6	0.7	50	12	US-10-029-630-6	Sequence 6, Appl1
309	15.8	0.7	50	10	US-09-504-231A-2973	Sequence 2973, Ap	c 382	15.6	0.7	50	12	US-09-969-373-1696	Sequence 1696, Ap
310	15.8	0.7	50	10	US-09-504-231A-2994	Sequence 2994, Ap	c 383	15.6	0.7	21	10	US-09-866-108-12651	Sequence 12651, A
311	15.8	0.7	50	10	US-09-504-231A-3028	Sequence 3028, Ap	c 384	15.4	0.7	25	10		

C 385	15.4	0.7	25	10	US-09-866-108-13695	Sequence 13695, A	C 458	15.4	0.7	50	10	US-09-504-231A-2987	Sequence 2987, Ap
C 386	15.4	0.7	25	10	US-09-866-108-13696	Sequence 13696, A	C 459	15.4	0.7	50	10	US-09-504-231A-2991	Sequence 2991, Ap
C 387	15.4	0.7	25	10	US-09-866-108-14966	Sequence 14966, A	C 460	15.4	0.7	50	10	US-09-504-231A-3014	Sequence 3014, Ap
C 388	15.4	0.7	25	10	US-09-866-108-15544	Sequence 15544, A	C 461	15.4	0.7	50	10	US-09-504-231A-3026	Sequence 3026, Ap
C 389	15.4	0.7	25	10	US-09-871-579-13	Sequence 13, Appl	C 462	15.4	0.7	50	10	US-09-504-231A-3096	Sequence 3096, Ap
C 390	15.4	0.7	25	10	US-09-843-007-4	Sequence 4, Appl	C 463	15.4	0.7	50	10	US-09-867-193-9	Sequence 9, Appl
C 391	15.4	0.7	27	10	US-09-334-923A-44	Sequence 44, Appl	C 464	15.4	0.7	50	10	US-09-274-553D-2915	Sequence 2915, Ap
C 392	15.4	0.7	27	10	US-09-975-901-8	Sequence 12, Appl	C 465	15.4	0.7	50	10	US-09-274-553D-2948	Sequence 2948, Ap
C 393	15.4	0.7	27	10	US-09-975-901-12	Sequence 44, Appl	C 466	15.4	0.7	50	10	US-09-274-553D-2971	Sequence 2971, Ap
C 394	15.4	0.7	27	10	US-09-334-954A-44	Sequence 44, Appl	C 467	15.4	0.7	50	10	US-09-274-553D-2987	Sequence 2987, Ap
C 395	15.4	0.7	27	10	US-09-334-954A-44	Sequence 44, Appl	C 468	15.4	0.7	50	10	US-09-274-553D-2991	Sequence 2991, Ap
C 396	15.4	0.7	29	10	US-09-756-095-93	Sequence 52, Appl	C 469	15.4	0.7	50	10	US-09-274-553D-3026	Sequence 3026, Ap
C 397	15.4	0.7	30	10	US-09-952-168-62	Sequence 52, Appl	C 470	15.4	0.7	50	10	US-09-274-553D-3026	Sequence 3026, Ap
C 398	15.4	0.7	31	10	US-09-272-162-5	Sequence 255, Ap	C 471	15.4	0.7	50	10	US-09-274-553D-3096	Sequence 3096, Ap
C 399	15.4	0.7	31	10	US-09-801-274-255	Sequence 1260, Ap	C 472	15.2	0.7	23	10	US-09-868-899-25	Sequence 3096, Ap
C 400	15.4	0.7	31	10	US-09-801-274-1260	Sequence 1311, Ap	C 473	15.2	0.7	24	10	US-09-868-899-25	Sequence 3096, Ap
C 401	15.4	0.7	32	10	US-09-801-274-1311	Sequence 10, Appl	C 474	15.2	0.7	24	10	US-09-868-899-25	Sequence 3096, Ap
C 402	15.4	0.7	33	10	US-09-894-698-12	Sequence 13, Appl	C 475	15.2	0.7	28	10	US-09-904-116-6	Sequence 14, Appl
C 403	15.4	0.7	33	10	US-09-333-966-10	Sequence 16, Appl	C 476	15.2	0.7	28	10	US-09-904-116-6	Sequence 14, Appl
C 404	15.4	0.7	33	10	US-09-333-966-13	Sequence 2, Appl	C 477	15.2	0.7	29	10	US-09-887-576-416	Sequence 10, Appl
C 405	15.4	0.7	33	12	US-10-108-280-2	Sequence 2, Appl	C 478	15.2	0.7	30	9	US-09-944-413-109	Sequence 416, Ap
C 406	15.4	0.7	34	9	US-09-826-025-22	Sequence 250, App	C 479	15.2	0.7	30	10	US-09-771-425-3	Sequence 109, Ap
C 407	15.4	0.7	34	10	US-09-765-272-250	Sequence 293, App	C 480	15.2	0.7	30	10	US-09-866-028-109	Sequence 109, Ap
C 408	15.4	0.7	34	10	US-09-765-272-293	Sequence 105, App	C 481	15.2	0.7	30	10	US-09-944-449-109	Sequence 109, Ap
C 409	15.4	0.7	35	10	US-09-920-552-105	Sequence 30, Appl	C 482	15.2	0.7	30	10	US-09-944-457-109	Sequence 109, Ap
C 410	15.4	0.7	35	12	US-10-139-262-30	Sequence 2341, Ap	C 483	15.2	0.7	30	10	US-09-945-587-109	Sequence 109, Ap
C 411	15.4	0.7	36	10	US-09-504-231A-2341	Sequence 280, App	C 484	15.2	0.7	30	10	US-09-945-587-109	Sequence 109, Ap
C 412	15.4	0.7	36	10	US-09-765-272-280	Sequence 2341, Ap	C 485	15.2	0.7	30	10	US-09-944-396-109	Sequence 109, Ap
C 413	15.4	0.7	36	10	US-09-765-272-280	Sequence 108, App	C 486	15.2	0.7	30	10	US-09-944-432-109	Sequence 109, Ap
C 414	15.4	0.7	37	10	US-09-755-665-108	Sequence 441, App	C 487	15.2	0.7	30	10	US-09-944-432-109	Sequence 109, Ap
C 415	15.4	0.7	38	10	US-09-765-272-441	Sequence 2, Appl	C 488	15.2	0.7	30	10	US-09-944-654-109	Sequence 109, Ap
C 416	15.4	0.7	38	10	US-09-944-243-2	Sequence 15, Appl	C 489	15.2	0.7	30	10	US-09-944-654-109	Sequence 109, Ap
C 417	15.4	0.7	38	10	US-09-874-389-15	Sequence 68, Appl	C 490	15.2	0.7	30	10	US-09-943-851A-109	Sequence 109, Ap
C 418	15.4	0.7	40	10	US-09-951-401-68	Sequence 1, Appl	C 491	15.2	0.7	31	9	US-10-029-905-7	Sequence 109, Ap
C 419	15.4	0.7	40	10	US-09-922-101-68	Sequence 32, Appl	C 492	15.2	0.7	31	10	US-09-801-274-990	Sequence 990, App
C 420	15.4	0.7	41	10	US-09-955-462A-1	Sequence 36, Appl	C 493	15.2	0.7	31	10	US-09-801-274-1451	Sequence 1451, Ap
C 421	15.4	0.7	42	9	US-09-966-140-32	Sequence 37, Appl	C 494	15.2	0.7	31	10	US-09-804-898-4	Sequence 4, Appl
C 422	15.4	0.7	44	9	US-09-793-139-36	Sequence 36, Appl	C 495	15.2	0.7	31	10	US-09-895-263-6	Sequence 16, Appl
C 423	15.4	0.7	44	9	US-09-793-139-36	Sequence 37, Appl	C 496	15.2	0.7	33	8	US-08-978-634-14	Sequence 14, Appl
C 424	15.4	0.7	44	10	US-09-818-879-36	Sequence 37, Appl	C 497	15.2	0.7	33	8	US-08-978-634-14	Sequence 14, Appl
C 425	15.4	0.7	44	10	US-09-818-879-36	Sequence 37, Appl	C 498	15.2	0.7	33	8	US-08-978-634-14	Sequence 14, Appl
C 426	15.4	0.7	44	10	US-09-211-755B-36	Sequence 37, Appl	C 499	15.2	0.7	33	8	US-08-978-634-14	Sequence 14, Appl
C 427	15.4	0.7	44	10	US-09-211-755B-36	Sequence 37, Appl	C 500	15.2	0.7	33	10	US-09-816-531A-2	Sequence 27, Appl
C 428	15.4	0.7	45	10	US-09-838-386-17	Sequence 17, Appl	C 501	15.2	0.7	34	10	US-09-923-246-27	Sequence 27, Appl
C 429	15.4	0.7	45	10	US-09-838-386-17	Sequence 18, Appl	C 502	15.2	0.7	35	9	US-09-923-246-27	Sequence 27, Appl
C 430	15.4	0.7	45	10	US-09-867-274-19	Sequence 19, Appl	C 503	15.2	0.7	35	10	US-09-773-599-14	Sequence 14, Appl
C 431	15.4	0.7	46	10	US-09-827-289-25	Sequence 25, Appl	C 504	15.2	0.7	35	10	US-09-773-599-14	Sequence 14, Appl
C 432	15.4	0.7	46	10	US-09-827-289-25	Sequence 25, Appl	C 505	15.2	0.7	35	10	US-09-773-599-14	Sequence 14, Appl
C 433	15.4	0.7	47	10	US-09-151-450-9	Sequence 9, Appl	C 506	15.2	0.7	36	8	US-08-424-550B-625	Sequence 12, Appl
C 434	15.4	0.7	47	10	US-09-901-484A-196	Sequence 196, App	C 507	15.2	0.7	36	10	US-09-943-215-7	Sequence 625, App
C 435	15.4	0.7	47	10	US-09-901-484A-244	Sequence 244, App	C 508	15.2	0.7	37	9	US-09-922-261-235	Sequence 235, App
C 436	15.4	0.7	47	10	US-09-901-484A-252	Sequence 252, App	C 509	15.2	0.7	38	10	US-09-922-261-235	Sequence 235, App
C 437	15.4	0.7	48	9	US-09-760-500A-29	Sequence 29, Appl	C 510	15.2	0.7	38	10	US-09-922-261-235	Sequence 235, App
C 438	15.4	0.7	48	9	US-09-767-409A-29	Sequence 29, Appl	C 511	15.2	0.7	39	10	US-09-727-311-26	Sequence 29, Appl
C 439	15.4	0.7	48	9	US-09-975-062A-29	Sequence 29, Appl	C 512	15.2	0.7	39	10	US-09-727-311-26	Sequence 29, Appl
C 440	15.4	0.7	48	9	US-09-975-062A-29	Sequence 29, Appl	C 513	15.2	0.7	39	10	US-09-727-311-26	Sequence 29, Appl
C 441	15.4	0.7	48	9	US-09-975-062A-29	Sequence 29, Appl	C 514	15.2	0.7	41	10	US-09-774-414-20	Sequence 20, Appl
C 442	15.4	0.7	48	9	US-09-975-062A-29	Sequence 29, Appl	C 515	15.2	0.7	41	10	US-09-774-414-20	Sequence 20, Appl
C 443	15.4	0.7	48	10	US-09-973-625-29	Sequence 29, Appl	C 516	15.2	0.7	42	10	US-09-923-246-27	Sequence 27, Appl
C 444	15.4	0.7	48	10	US-09-973-625-29	Sequence 29, Appl	C 517	15.2	0.7	42	10	US-09-923-246-27	Sequence 27, Appl
C 445	15.4	0.7	48	10	US-09-973-625-29	Sequence 29, Appl	C 518	15.2	0.7	42	10	US-09-923-246-27	Sequence 27, Appl
C 446	15.4	0.7	48	10	US-09-973-625-29	Sequence 29, Appl	C 519	15.2	0.7	42	10	US-09-923-246-27	Sequence 27, Appl
C 447	15.4	0.7	48	10	US-09-973-625-29	Sequence 29, Appl	C 520	15.2	0.7	42	10	US-09-923-246-27	Sequence 27, Appl
C 448	15.4	0.7	48	10	US-09-973-625-29	Sequence 29, Appl	C 521	15.2	0.7	43	10	US-09-923-246-27	Sequence 27, Appl
C 449	15.4	0.7	48	10	US-09-973-625-29	Sequence 29, Appl	C 522	15.2	0.7	43	10	US-09-923-246-27	Sequence 27, Appl
C 450	15.4	0.7	49	10	US-09-973-625-29	Sequence 29, Appl	C 523	15.2	0.7	44	10	US-09-923-246-27	Sequence 27, Appl
C 451	15.4	0.7	49	10	US-09-973-625-29	Sequence 29, Appl	C 524	15.2	0.7	44	10	US-09-923-246-27	Sequence 27, Appl
C 452	15.4	0.7	50	9	US-09-978-295A-408	Sequence 14, Appl	C 525	15.2	0.7	44	10	US-09-923-246-27	Sequence 27, Appl
C 453	15.4	0.7	50	9	US-09-978-295A-408	Sequence 14, Appl	C 526	15.2	0.7	44	10	US-09-923-246-27	Sequence 27, Appl
C 454	15.4	0.7	50	10	US-09-790-417-279	Sequence 279, App	C 527	15.2	0.7	44	10	US-09-923-246-27	Sequence 27, Appl
C 455	15.4	0.7	50	10	US-09-815-343-1012	Sequence 1012, App	C 528	15.2	0.7	44	10	US-09-923-246-27	Sequence 27, Appl
C 456	15.4	0.7	50	10	US-09-504-231A-2915	Sequence 2915, Ap	C 529	15.2	0.7	46	10	US-09-844-265-22	Sequence 22, Appl
C 457	15.4	0.7	50	10	US-09-504-231A-2948	Sequence 2948, Ap	C 530	15.2	0.7	46	10	US-09-844-265-22	Sequence 22, Appl
					Sequence 2971, Ap							US-09-835-147-21	Sequence 21, Appl

531	15.2	0.7	46	10	US-09-827-289-22	Sequence 22, Appl	604	15	0.6	25	10	US-09-866-108-15408	Sequence 15408, A
C 532	15.2	0.7	47	9	US-09-995-749A-9	Sequence 9, Appl1	605	15	0.6	25	10	US-09-263-959-876	Sequence 876, App
C 533	15.2	0.7	47	10	US-09-822-250-35	Sequence 35, Appl	606	15	0.6	25	10	US-09-263-689-46	Sequence 46, Appl
534	15.2	0.7	47	10	US-09-817-014-19	Sequence 19, Appl	607	15	0.6	26	10	US-09-179-536B-134	Sequence 134, App
535	15.2	0.7	47	10	US-09-901-484A-220	Sequence 220, App	608	15	0.6	27	12	US-10-139-672-15	Sequence 15, Appl
536	15.2	0.7	47	10	US-09-901-484A-235	Sequence 235, App	609	15	0.6	28	12	US-10-005-073-4	Sequence 4, Appl1
C 537	15.2	0.7	47	10	US-09-901-484A-284	Sequence 284, App	610	15	0.6	28	12	US-10-005-073-6	Sequence 6, Appl1
538	15.2	0.7	47	10	US-09-901-484A-312	Sequence 312, App	611	15	0.6	29	10	US-09-179-536B-133	Sequence 133, App
C 539	15.2	0.7	48	9	US-09-905-291A-357	Sequence 357, App	612	15	0.6	29	10	US-09-179-536B-135	Sequence 135, App
C 540	15.2	0.7	48	10	US-09-284-665A-20	Sequence 20, Appl	C 613	15	0.6	30	9	US-09-924-097-10	Sequence 10, Appl
C 541	15.2	0.7	48	10	US-09-810-502-29	Sequence 29, Appl	614	15	0.6	30	10	US-09-825-301-61	Sequence 61, Appl
C 542	15.2	0.7	48	10	US-09-909-320-357	Sequence 357, App	615	15	0.6	30	10	US-09-989-441-15	Sequence 15, Appl
C 543	15.2	0.7	48	10	US-09-909-088B-357	Sequence 357, App	616	15	0.6	31	10	US-09-801-274-1636	Sequence 1636, App
C 544	15.2	0.7	49	10	US-09-900-062-43	Sequence 43, Appl	617	15	0.6	31	10	US-09-179-536B-139	Sequence 139, App
545	15.2	0.7	50	9	US-09-996-956-6	Sequence 6, Appl1	618	15	0.6	31	10	US-09-905-173-8	Sequence 8, Appl1
546	15.2	0.7	50	9	US-09-905-291A-270	Sequence 270, App	619	15	0.6	32	9	US-09-319-264-1	Sequence 1, Appl1
C 547	15.2	0.7	50	9	US-09-992-598-50	Sequence 270, App	620	15	0.6	32	10	US-09-814-786-37	Sequence 37, Appl
548	15.2	0.7	50	10	US-09-790-417-279	Sequence 279, App	C 621	15	0.6	32	10	US-09-804-682-89	Sequence 89, Appl
549	15.2	0.7	50	10	US-09-790-417-280	Sequence 280, App	622	15	0.6	32	10	US-09-804-682-92	Sequence 92, Appl
C 550	15.2	0.7	50	10	US-09-504-231A-2923	Sequence 2923, App	C 623	15	0.6	33	10	US-09-426-548-15	Sequence 15, Appl
C 551	15.2	0.7	50	10	US-09-504-231A-2936	Sequence 2936, App	624	15	0.6	33	10	US-09-930-251-10	Sequence 10, Appl
C 552	15.2	0.7	50	10	US-09-504-231A-2953	Sequence 2953, App	C 625	15	0.6	33	10	US-09-804-682-86	Sequence 86, Appl
C 553	15.2	0.7	50	10	US-09-504-231A-2972	Sequence 2972, App	626	15	0.6	33	10	US-09-804-682-93	Sequence 93, Appl
C 554	15.2	0.7	50	10	US-09-504-231A-3038	Sequence 3038, App	627	15	0.6	33	10	US-09-263-689-47	Sequence 47, Appl
C 555	15.2	0.7	50	10	US-09-504-231A-3042	Sequence 3042, App	628	15	0.6	33	10	US-09-263-689-54	Sequence 54, Appl
C 556	15.2	0.7	50	10	US-09-504-231A-3049	Sequence 3049, App	C 629	15	0.6	34	9	US-09-771-009-27	Sequence 27, Appl
C 557	15.2	0.7	50	10	US-09-504-231A-3059	Sequence 3059, App	630	15	0.6	34	10	US-09-766-095-16	Sequence 36, Appl
C 558	15.2	0.7	50	10	US-09-504-231A-3084	Sequence 3084, App	631	15	0.6	34	10	US-09-925-365B-7	Sequence 116, App
C 559	15.2	0.7	50	10	US-09-504-231A-3091	Sequence 3091, App	C 632	15	0.6	34	10	US-09-884-814-3	Sequence 7, Appl1
C 560	15.2	0.7	50	10	US-09-504-231A-3095	Sequence 3095, App	633	15	0.6	35	10	US-09-790-399-15	Sequence 3, Appl1
C 561	15.2	0.7	50	10	US-09-504-231A-3107	Sequence 3107, App	C 634	15	0.6	35	10	US-09-915-060-14	Sequence 14, Appl
562	15.2	0.7	50	10	US-09-841-132-207	Sequence 207, App	635	15	0.6	35	10	US-09-915-060-16	Sequence 16, Appl
C 563	15.2	0.7	50	10	US-09-989-722-50	Sequence 50, Appl	636	15	0.6	35	10	US-09-835-147-19	Sequence 19, Appl
C 564	15.2	0.7	50	10	US-09-989-722-50	Sequence 50, Appl	C 637	15	0.6	36	10	US-09-120-064-7	Sequence 7, Appl1
C 565	15.2	0.7	50	10	US-09-989-729-50	Sequence 50, Appl	638	15	0.6	37	10	US-09-952-572-6	Sequence 6, Appl1
C 566	15.2	0.7	50	10	US-09-989-727-50	Sequence 50, Appl	C 639	15	0.6	37	10	US-09-948-41A-1	Sequence 1, Appl1
C 567	15.2	0.7	50	10	US-09-274-553D-2923	Sequence 2923, App	C 640	15	0.6	37	10	US-09-818-879-33	Sequence 33, Appl
C 568	15.2	0.7	50	10	US-09-274-553D-2936	Sequence 2936, App	641	15	0.6	38	9	US-09-793-139-33	Sequence 3, Appl
C 569	15.2	0.7	50	10	US-09-274-553D-2953	Sequence 2953, App	642	15	0.6	38	10	US-09-179-536B-136	Sequence 136, App
570	15.2	0.7	50	10	US-09-274-553D-2972	Sequence 2972, App	643	15	0.6	38	10	US-09-211-755B-13	Sequence 33, Appl
C 571	15.2	0.7	50	10	US-09-274-553D-3038	Sequence 3038, App	644	15	0.6	38	10	US-09-766-095-37	Sequence 37, Appl
C 572	15.2	0.7	50	10	US-09-274-553D-3042	Sequence 3042, App	C 645	15	0.6	38	10	US-09-766-095-117	Sequence 117, App
C 573	15.2	0.7	50	10	US-09-274-553D-3049	Sequence 3049, App	C 646	15	0.6	38	10	US-09-885-478-11	Sequence 11, Appl
C 574	15.2	0.7	50	10	US-09-274-553D-3059	Sequence 3059, App	647	15	0.6	38	10	US-09-888-049-10	Sequence 10, Appl
C 575	15.2	0.7	50	10	US-09-274-553D-3084	Sequence 3084, App	C 648	15	0.6	38	10	US-09-870-122-15	Sequence 15, Appl
C 576	15.2	0.7	50	10	US-09-274-553D-3091	Sequence 3091, App	649	15	0.6	38	10	US-10-007-448-3	Sequence 3, Appl1
C 577	15.2	0.7	50	10	US-09-274-553D-3095	Sequence 3095, App	C 650	15	0.6	38	12	US-09-771-009-24	Sequence 24, Appl
C 578	15.2	0.7	50	10	US-09-989-731-50	Sequence 3107, App	C 651	15	0.6	39	9	US-09-753-436-109	Sequence 109, App
C 579	15.2	0.7	50	10	US-09-989-732-50	Sequence 50, Appl	C 652	15	0.6	39	10	US-09-987-456-144	Sequence 144, App
C 580	15.2	0.7	50	10	US-09-989-732-50	Sequence 50, Appl	C 653	15	0.6	39	10	US-09-987-456-144	Sequence 144, App
C 581	15.2	0.7	50	10	US-09-989-732-50	Sequence 50, Appl	C 654	15	0.6	39	10	US-10-066-151-62	Sequence 62, Appl
582	15.2	0.7	50	10	US-09-909-320-270	Sequence 270, App	C 655	15	0.6	39	12	US-09-996-140-28	Sequence 28, Appl
C 583	15.2	0.7	50	10	US-09-990-442-50	Sequence 50, Appl	C 656	15	0.6	40	9	US-09-765-272-253	Sequence 253, App
C 584	15.2	0.7	50	10	US-09-991-163-50	Sequence 50, Appl	657	15	0.6	40	10	US-09-842-164-20	Sequence 20, Appl
C 585	15.2	0.7	50	10	US-09-993-604-50	Sequence 50, Appl	658	15	0.6	40	10	US-09-924-154-10	Sequence 10, Appl
C 586	15.2	0.7	50	10	US-09-990-456-50	Sequence 50, Appl	659	15	0.6	40	10	US-09-910-120-10	Sequence 10, Appl
C 587	15.2	0.7	50	10	US-09-989-721-50	Sequence 50, Appl	660	15	0.6	41	10	US-09-920-581-9	Sequence 9, Appl1
588	15.2	0.7	50	10	US-09-909-088B-270	Sequence 270, App	661	15	0.6	41	10	US-09-771-009-26	Sequence 26, Appl
C 589	15	0.6	21	10	US-09-888-243-10	Sequence 10, Appl	662	15	0.6	42	9	US-09-887-880-15	Sequence 15, Appl
C 590	15	0.6	23	10	US-09-927-602-35	Sequence 35, Appl	C 663	15	0.6	42	9	US-09-978-295A-243	Sequence 243, App
C 591	15	0.6	23	10	US-09-777-430A-18	Sequence 18, Appl	664	15	0.6	42	9	US-09-904-380-12	Sequence 12, Appl
C 592	15	0.6	24	10	US-09-923-684-11	Sequence 11, Appl	665	15	0.6	42	10	US-09-824-568-3	Sequence 3, Appl1
C 593	15	0.6	24	10	US-09-779-307-42	Sequence 42, Appl	666	15	0.6	43	10	US-09-732-561-11	Sequence 11, Appl
594	15	0.6	25	10	US-09-866-108-12652	Sequence 12652, A	667	15	0.6	43	10	US-09-732-348-9	Sequence 9, Appl1
595	15	0.6	25	10	US-09-866-108-12653	Sequence 12653, A	668	15	0.6	44	10	US-09-292-9273-14	Sequence 14, Appl
C 596	15	0.6	25	10	US-09-866-108-13692	Sequence 13692, A	C 669	15	0.6	45	9	US-09-729-520-4	Sequence 4, Appl1
597	15	0.6	25	10	US-09-866-108-14867	Sequence 14867, A	670	15	0.6	45	9	US-10-008-620-4	Sequence 4, Appl1
598	15	0.6	25	10	US-09-866-108-14868	Sequence 14868, A	671	15	0.6	45	10	US-09-828-592-5	Sequence 5, Appl1
599	15	0.6	25	10	US-09-866-108-14869	Sequence 14869, A	C 672	15	0.6	45	10	US-09-827-289-18	Sequence 18, Appl
600	15	0.6	25	10	US-09-866-108-14872	Sequence 14872, A	C 673	15	0.6	45	10	US-09-818-066-32	Sequence 32, Appl
601	15	0.6	25	10	US-09-866-108-14873	Sequence 14873, A	C 674	15	0.6	45	10	US-09-848-164-104	Sequence 104, App
602	15	0.6	25	10	US-09-866-108-14874	Sequence 14874, A	675	15	0.6	46	10	US-09-320-337-38	Sequence 38, Appl
603	15	0.6	25	10	US-09-866-108-15405	Sequence 15405, A	C 676	15	0.6	46	10		

677	15	0.6	46	10	US-09-827-289-20	Sequence 20, Appl	750	14.8	0.6	29	12	US-10-040-916-64	Sequence 64, Appl
678	15	0.6	46	10	US-09-932-679-22	Sequence 22, Appl	751	14.8	0.6	30	10	US-09-725-735A-9	Sequence 9, Appl1
679	15	0.6	47	10	US-09-804-682-108	Sequence 108, App	752	14.8	0.6	30	10	US-09-853-053-4	Sequence 4, Appl1
680	15	0.6	47	10	US-09-901-484A-210	Sequence 210, App	753	14.8	0.6	30	10	US-09-853-053-5	Sequence 5, Appl1
681	15	0.6	47	10	US-09-901-484A-219	Sequence 219, App	754	14.8	0.6	30	10	US-09-853-053-12	Sequence 12, Appl
682	15	0.6	47	10	US-09-901-484A-231	Sequence 231, App	755	14.8	0.6	30	10	US-09-760-574-5	Sequence 5, Appl1
683	15	0.6	47	10	US-09-901-484A-247	Sequence 247, App	756	14.8	0.6	30	10	US-09-777-40A-21	Sequence 21, Appl
684	15	0.6	47	10	US-09-901-484A-308	Sequence 308, App	757	14.8	0.6	31	10	US-09-801-274-673	Sequence 673, App
685	15	0.6	47	10	US-09-901-484A-311	Sequence 311, App	758	14.8	0.6	31	10	US-09-801-274-1346	Sequence 1346, App
686	15	0.6	48	10	US-09-755-747A-1	Sequence 1, Appl1	759	14.8	0.6	31	10	US-09-801-274-1625	Sequence 1625, App
687	15	0.6	48	10	US-09-351-819-2	Sequence 16, Appl	761	14.8	0.6	31	10	US-09-801-274-1771	Sequence 1771, App
688	15	0.6	48	12	US-10-091-085-16	Sequence 91, Appl	762	14.8	0.6	31	10	US-09-885-478-18	Sequence 18, Appl
689	15	0.6	49	9	US-09-987-107-91	Sequence 238, App	763	14.8	0.6	32	8	US-09-885-478-19	Sequence 17, Appl
690	15	0.6	49	9	US-09-905-291A-380	Sequence 380, App	764	14.8	0.6	32	12	US-08-945-038-17	Sequence 17, Appl
691	15	0.6	49	9	US-09-905-291A-388	Sequence 27, Appl	765	14.8	0.6	33	9	US-10-013-718-1	Sequence 1, Appl1
692	15	0.6	49	10	US-09-781-902-27	Sequence 43, Appl	766	14.8	0.6	33	10	US-09-927-886-16	Sequence 16, Appl
693	15	0.6	49	10	US-09-900-062-43	Sequence 238, App	767	14.8	0.6	33	10	US-09-927-886-16	Sequence 16, Appl
694	15	0.6	49	10	US-09-920-320-338	Sequence 43, Appl	768	14.8	0.6	34	10	US-09-792-439-6	Sequence 9, Appl1
695	15	0.6	49	10	US-09-909-320-380	Sequence 380, App	769	14.8	0.6	34	10	US-09-784-982-9	Sequence 9, Appl1
696	15	0.6	49	10	US-09-758-525A-12	Sequence 12, Appl	770	14.8	0.6	34	10	US-09-419-305-9	Sequence 9, Appl1
697	15	0.6	49	10	US-09-944-243-1	Sequence 1, Appl1	771	14.8	0.6	34	10	US-09-931-186-13	Sequence 13, Appl
698	15	0.6	49	10	US-09-909-088B-238	Sequence 238, App	772	14.8	0.6	34	10	US-09-931-186-24	Sequence 24, Appl
699	15	0.6	49	10	US-09-909-088B-380	Sequence 380, App	773	14.8	0.6	34	10	US-09-263-959-803	Sequence 803, App
700	15	0.6	50	9	US-09-801-371A-9	Sequence 9, Appl1	774	14.8	0.6	35	8	US-10-045-428A-11	Sequence 11, Appl
701	15	0.6	50	10	US-09-790-417-277	Sequence 277, App	775	14.8	0.6	35	9	US-08-961-888-31	Sequence 31, Appl
702	15	0.6	50	10	US-09-790-417-278	Sequence 277, App	776	14.8	0.6	35	10	US-09-811-088-13	Sequence 13, Appl
703	15	0.6	50	10	US-09-790-417-280	Sequence 280, App	777	14.8	0.6	35	10	US-09-727-311-22	Sequence 22, Appl
704	15	0.6	50	10	US-09-504-231A-3003	Sequence 3003, App	778	14.8	0.6	35	10	US-09-732-61-2	Sequence 2, Appl1
705	15	0.6	50	10	US-09-504-231A-3019	Sequence 3019, App	779	14.8	0.6	35	10	US-09-732-61-2	Sequence 2, Appl1
706	15	0.6	50	10	US-09-504-231A-3029	Sequence 3029, App	780	14.8	0.6	35	10	US-09-842-552-27	Sequence 27, Appl
707	15	0.6	50	10	US-09-504-231A-3047	Sequence 3047, App	781	14.8	0.6	36	8	US-09-971-309-36	Sequence 36, Appl
708	15	0.6	50	10	US-09-504-231A-3060	Sequence 3060, App	782	14.8	0.6	36	8	US-08-786-531B-7	Sequence 7, Appl1
709	15	0.6	50	10	US-09-504-231A-3065	Sequence 3065, App	783	14.8	0.6	36	10	US-08-424-550B-641	Sequence 64, App
710	15	0.6	50	10	US-09-504-231A-3066	Sequence 3066, App	784	14.8	0.6	36	10	US-09-426-548-112	Sequence 112, App
711	15	0.6	50	10	US-09-504-231A-3068	Sequence 3068, App	785	14.8	0.6	36	10	US-09-426-548-115	Sequence 115, App
712	15	0.6	50	10	US-09-909-496-1	Sequence 1, Appl1	786	14.8	0.6	36	10	US-09-735-450-9	Sequence 9, Appl1
713	15	0.6	50	10	US-09-909-496-10	Sequence 10, Appl1	787	14.8	0.6	36	10	US-09-903-456-11	Sequence 11, App
714	15	0.6	50	10	US-09-909-496-10	Sequence 3, Appl1	788	14.8	0.6	37	9	US-10-127-733-7	Sequence 7, Appl1
715	15	0.6	50	10	US-09-924-553D-3003	Sequence 3003, App	789	14.8	0.6	37	10	US-09-989-722-463	Sequence 463, App
716	15	0.6	50	10	US-09-274-553D-3019	Sequence 3019, App	790	14.8	0.6	37	10	US-09-989-723-463	Sequence 463, App
717	15	0.6	50	10	US-09-274-553D-3029	Sequence 3029, App	791	14.8	0.6	37	10	US-09-989-729-463	Sequence 463, App
718	15	0.6	50	10	US-09-274-553D-3047	Sequence 3047, App	792	14.8	0.6	37	10	US-09-989-727-463	Sequence 463, App
719	15	0.6	50	10	US-09-274-553D-3060	Sequence 3060, App	793	14.8	0.6	37	10	US-09-989-731-463	Sequence 463, App
720	15	0.6	50	10	US-09-274-553D-3065	Sequence 3065, App	794	14.8	0.6	37	10	US-09-989-732-463	Sequence 463, App
721	15	0.6	50	10	US-09-274-553D-3085	Sequence 3085, App	795	14.8	0.6	37	10	US-09-989-732-463	Sequence 463, App
722	15	0.6	50	10	US-09-776-529A-3	Sequence 3, Appl1	796	14.8	0.6	37	10	US-09-921-073-463	Sequence 463, App
723	15	0.6	50	10	US-09-776-529A-3	Sequence 2759, App	797	14.8	0.6	37	10	US-09-920-442-463	Sequence 463, App
724	15	0.6	50	10	US-09-776-529A-3	Sequence 15, Appl	798	14.8	0.6	37	10	US-09-921-163-463	Sequence 463, App
725	15	0.6	50	10	US-09-849-014-14	Sequence 15, Appl1	799	14.8	0.6	37	10	US-09-921-163-463	Sequence 463, App
726	15	0.6	50	10	US-09-849-014-14	Sequence 48, Appl1	800	14.8	0.6	37	10	US-09-933-604-463	Sequence 463, App
727	15	0.6	50	10	US-09-849-014-14	Sequence 14, Appl1	801	14.8	0.6	38	10	US-09-989-721-463	Sequence 463, App
728	15	0.6	50	10	US-09-849-014-14	Sequence 14, Appl1	802	14.8	0.6	38	10	US-09-989-721-463	Sequence 463, App
729	15	0.6	50	10	US-09-849-014-14	Sequence 14, Appl1	803	14.8	0.6	38	10	US-09-989-721-463	Sequence 463, App
730	15	0.6	50	10	US-09-849-014-14	Sequence 14, Appl1	804	14.8	0.6	38	10	US-09-989-721-463	Sequence 463, App
731	15	0.6	50	10	US-09-849-014-14	Sequence 14, Appl1	805	14.8	0.6	38	10	US-09-989-721-463	Sequence 463, App
732	15	0.6	50	10	US-09-849-014-14	Sequence 14, Appl1	806	14.8	0.6	39	10	US-09-989-721-463	Sequence 463, App
733	15	0.6	50	10	US-09-849-014-14	Sequence 14, Appl1	807	14.8	0.6	39	10	US-09-989-721-463	Sequence 463, App
734	15	0.6	50	10	US-09-849-014-14	Sequence 14, Appl1	808	14.8	0.6	39	10	US-09-989-721-463	Sequence 463, App
735	15	0.6	50	10	US-09-849-014-14	Sequence 14, Appl1	809	14.8	0.6	39	10	US-09-989-721-463	Sequence 463, App
736	15	0.6	50	10	US-09-849-014-14	Sequence 14, Appl1	810	14.8	0.6	39	10	US-09-989-721-463	Sequence 463, App
737	15	0.6	50	10	US-09-849-014-14	Sequence 14, Appl1	811	14.8	0.6	39	10	US-09-989-721-463	Sequence 463, App
738	15	0.6	50	10	US-09-849-014-14	Sequence 14, Appl1	812	14.8	0.6	40	9	US-09-924-558-324	Sequence 324, App
739	15	0.6	50	10	US-09-849-014-14	Sequence 14, Appl1	813	14.8	0.6	40	10	US-09-924-558-324	Sequence 324, App
740	15	0.6	50	10	US-09-849-014-14	Sequence 14, Appl1	814	14.8	0.6	40	10	US-09-924-558-324	Sequence 324, App
741	15	0.6	50	10	US-09-849-014-14	Sequence 14, Appl1	815	14.8	0.6	40	10	US-09-924-558-324	Sequence 324, App
742	15	0.6	50	10	US-09-849-014-14	Sequence 14, Appl1	816	14.8	0.6	40	10	US-09-924-558-324	Sequence 324, App
743	15	0.6	50	10	US-09-849-014-14	Sequence 14, Appl1	817	14.8	0.6	40	10	US-09-924-558-324	Sequence 324, App
744	15	0.6	50	10	US-09-849-014-14	Sequence 14, Appl1	818	14.8	0.6	40	10	US-09-924-558-324	Sequence 324, App
745	15	0.6	50	10	US-09-849-014-14	Sequence 14, Appl1	819	14.8	0.6	40	10	US-09-924-558-324	Sequence 324, App
746	15	0.6	50	10	US-09-849-014-14	Sequence 14, Appl1	820	14.8	0.6	40	10	US-09-924-558-324	Sequence 324, App
747	15	0.6	50	10	US-09-849-014-14	Sequence 14, Appl1	821	14.8	0.6	40	10	US-09-924-558-324	Sequence 324, App
748	15	0.6	50	10	US-09-849-014-14	Sequence 14, Appl1	822	14.8	0.6	40	10	US-09-924-558-324	Sequence 324, App
749	15	0.6	50	10	US-09-849-014-14	Sequence 14, Appl1	822	14.8	0.6	40	10	US-09-924-558-324	Sequence 324, App

C 823	14.8	0.6	40	10	US-09-990-456-324	Sequence 324, App	896	14.8	0.6	50	10	US-09-989-731-144	Sequence 144, App
C 824	14.8	0.6	40	10	US-09-989-721-324	Sequence 324, App	897	14.8	0.6	50	10	US-09-264-4688-7	Sequence 7, Appl1
C 825	14.8	0.6	40	10	US-09-263-959-221	Sequence 221, App	898	14.8	0.6	50	10	US-09-912-787-19	Sequence 19, Appl1
C 826	14.8	0.6	41	10	US-09-765-272-331	Sequence 331, App	899	14.8	0.6	50	10	US-09-989-732-144	Sequence 144, App
C 827	14.8	0.6	41	10	US-09-908-855-31	Sequence 31, App	900	14.8	0.6	50	10	US-09-991-073-144	Sequence 144, App
C 828	14.8	0.6	41	10	US-09-823-829-45	Sequence 45, Appl1	C 901	14.8	0.6	50	10	US-09-909-320-79	Sequence 79, Appl1
C 829	14.8	0.6	42	10	US-09-810-502-21	Sequence 21, Appl1	C 902	14.8	0.6	50	10	US-09-990-442-144	Sequence 144, App
C 830	14.8	0.6	42	10	US-09-826-312-16	Sequence 16, Appl1	C 903	14.8	0.6	50	10	US-09-991-163-144	Sequence 144, App
C 831	14.8	0.6	42	10	US-09-780-662A-23	Sequence 23, Appl1	C 904	14.8	0.6	50	10	US-09-993-604-144	Sequence 144, App
C 832	14.8	0.6	42	10	US-09-873-737A-8	Sequence 8, Appl1	C 905	14.8	0.6	50	10	US-09-990-456-144	Sequence 144, App
C 833	14.8	0.6	42	10	US-09-954-737-20	Sequence 20, Appl1	C 906	14.8	0.6	50	10	US-09-944-243-5	Sequence 5, Appl1
C 834	14.8	0.6	43	10	US-09-771-425-12	Sequence 12, Appl1	C 907	14.8	0.6	50	10	US-09-989-721-144	Sequence 144, App
C 835	14.8	0.6	43	10	US-09-771-425-13	Sequence 13, Appl1	C 908	14.8	0.6	50	10	US-09-909-088B-79	Sequence 79, Appl1
C 836	14.8	0.6	43	10	US-09-746-359A-50	Sequence 50, Appl1	C 909	14.8	0.6	50	12	US-10-014-326-5	Sequence 5, Appl1
C 837	14.8	0.6	43	10	US-09-825-561A-61	Sequence 61, Appl1	C 910	14.6	0.6	21	10	US-09-946-805-10	Sequence 10, Appl1
C 838	14.8	0.6	45	8	US-08-973-028-6	Sequence 6, Appl1	C 911	14.6	0.6	22	10	US-09-853-830-126	Sequence 126, App
C 839	14.8	0.6	45	9	US-09-925-664-73	Sequence 73, Appl1	C 912	14.6	0.6	22	10	US-09-969-373-2202	Sequence 2202, App
C 840	14.8	0.6	45	10	US-09-732-914-123	Sequence 123, App	C 913	14.6	0.6	22	10	US-09-969-373-2706	Sequence 2706, App
C 841	14.8	0.6	45	10	US-09-827-289-12	Sequence 12, Appl1	C 914	14.6	0.6	24	10	US-09-791-500-14	Sequence 14, Appl1
C 842	14.8	0.6	45	10	US-09-842-552-49	Sequence 49, Appl1	C 915	14.6	0.6	24	10	US-09-215-652-39	Sequence 39, Appl1
C 843	14.8	0.6	45	10	US-09-065-040-23	Sequence 23, Appl1	C 916	14.6	0.6	24	10	US-09-740-668A-79	Sequence 79, Appl1
C 844	14.8	0.6	45	10	US-09-969-192-42	Sequence 42, Appl1	C 917	14.6	0.6	24	10	US-09-995-542-17	Sequence 17, Appl1
C 845	14.8	0.6	45	12	US-10-002-278-14	Sequence 14, Appl1	C 918	14.6	0.6	24	10	US-09-969-373-1623	Sequence 1623, App
C 846	14.8	0.6	46	9	US-10-106-092-6	Sequence 6, Appl1	C 919	14.6	0.6	25	10	US-09-864-680-7	Sequence 7, Appl1
C 847	14.8	0.6	46	9	US-09-835-147-21	Sequence 21, Appl1	C 920	14.6	0.6	25	10	US-09-866-108-10839	Sequence 10839, A
C 848	14.8	0.6	46	10	US-09-848-164-67	Sequence 67, Appl1	C 921	14.6	0.6	25	10	US-09-866-108-10840	Sequence 10840, A
C 849	14.8	0.6	46	10	US-09-848-164-68	Sequence 68, Appl1	C 922	14.6	0.6	25	10	US-09-866-108-10841	Sequence 10841, A
C 850	14.8	0.6	46	10	US-09-848-164-68	Sequence 68, Appl1	C 923	14.6	0.6	25	10	US-09-866-108-10842	Sequence 10842, A
C 851	14.8	0.6	46	10	US-09-419-305-14	Sequence 14, Appl1	C 924	14.6	0.6	25	10	US-09-866-108-10843	Sequence 10843, A
C 852	14.8	0.6	47	9	US-09-905-291A-358	Sequence 358, App	C 925	14.6	0.6	25	10	US-09-866-108-11912	Sequence 11912, A
C 853	14.8	0.6	47	10	US-09-886-942-35	Sequence 35, Appl1	C 926	14.6	0.6	25	10	US-09-866-108-11913	Sequence 11913, A
C 854	14.8	0.6	47	10	US-09-817-014-19	Sequence 19, Appl1	C 927	14.6	0.6	25	10	US-09-866-108-11914	Sequence 11914, A
C 855	14.8	0.6	47	10	US-09-901-484A-286	Sequence 286, App	C 928	14.6	0.6	25	10	US-09-866-108-11915	Sequence 11915, A
C 856	14.8	0.6	47	10	US-09-901-484A-334	Sequence 334, App	C 929	14.6	0.6	25	10	US-09-866-108-11916	Sequence 11916, A
C 857	14.8	0.6	47	10	US-09-909-320-358	Sequence 358, App	C 930	14.6	0.6	25	10	US-09-866-108-13343	Sequence 13343, A
C 858	14.8	0.6	47	10	US-09-909-088B-358	Sequence 358, App	C 931	14.6	0.6	25	10	US-09-866-108-13344	Sequence 13344, A
C 859	14.8	0.6	47	10	US-09-263-959-138	Sequence 138, App	C 932	14.6	0.6	25	10	US-09-866-108-13345	Sequence 13345, A
C 860	14.8	0.6	48	9	US-09-944-413-119	Sequence 119, App	C 933	14.6	0.6	25	10	US-09-866-108-13346	Sequence 13346, A
C 861	14.8	0.6	48	10	US-09-790-399-23	Sequence 23, Appl1	C 934	14.6	0.6	25	10	US-09-866-108-13347	Sequence 13347, A
C 862	14.8	0.6	48	10	US-09-866-028-119	Sequence 119, App	C 935	14.6	0.6	25	10	US-09-866-108-15403	Sequence 15403, A
C 863	14.8	0.6	48	10	US-09-944-448-119	Sequence 119, App	C 936	14.6	0.6	25	10	US-09-866-108-15404	Sequence 15404, A
C 864	14.8	0.6	48	10	US-09-944-457-119	Sequence 119, App	C 937	14.6	0.6	25	10	US-09-750-373-49	Sequence 49, Appl1
C 865	14.8	0.6	48	10	US-09-916-940-74	Sequence 74, Appl1	C 938	14.6	0.6	26	10	US-09-910-428-2	Sequence 2, Appl1
C 866	14.8	0.6	48	10	US-09-945-587-119	Sequence 119, App	C 939	14.6	0.6	27	10	US-09-949-713-7	Sequence 7, Appl1
C 867	14.8	0.6	48	10	US-09-945-015-119	Sequence 119, App	C 940	14.6	0.6	28	10	US-09-887-576-372	Sequence 372, App
C 868	14.8	0.6	48	10	US-09-944-396-119	Sequence 119, App	C 941	14.6	0.6	28	8	US-08-834-666A-47	Sequence 47, Appl1
C 869	14.8	0.6	48	10	US-09-944-097-119	Sequence 119, App	C 942	14.6	0.6	29	9	US-09-863-040-49	Sequence 49, Appl1
C 870	14.8	0.6	48	10	US-09-944-432-119	Sequence 119, App	C 943	14.6	0.6	29	10	US-09-836-607-13	Sequence 13, Appl1
C 871	14.8	0.6	48	10	US-09-943-762-119	Sequence 119, App	C 944	14.6	0.6	29	10	US-09-836-607-15	Sequence 15, Appl1
C 872	14.8	0.6	48	10	US-09-944-654-119	Sequence 119, App	C 945	14.6	0.6	29	10	US-09-836-607-19	Sequence 19, Appl1
C 873	14.8	0.6	48	10	US-09-918-601-74	Sequence 74, Appl1	C 946	14.6	0.6	29	10	US-09-940-037A-21	Sequence 21, Appl1
C 874	14.8	0.6	48	10	US-09-943-851A-119	Sequence 119, App	C 947	14.6	0.6	29	12	US-10-040-916-58	Sequence 58, Appl1
C 875	14.8	0.6	49	9	US-09-905-291A-8	Sequence 8, Appl1	C 948	14.6	0.6	29	8	US-08-834-666A-44	Sequence 44, Appl1
C 876	14.8	0.6	49	10	US-09-740-002-10	Sequence 10, Appl1	C 949	14.6	0.6	30	8	US-09-840-243B-5	Sequence 5, Appl1
C 877	14.8	0.6	49	10	US-09-056-160B-43	Sequence 43, Appl1	C 950	14.6	0.6	30	9	US-09-879-813-6	Sequence 6, Appl1
C 878	14.8	0.6	49	10	US-09-922-958-6	Sequence 6, Appl1	C 951	14.6	0.6	30	9	US-09-966-955A-10	Sequence 10, Appl1
C 879	14.8	0.6	49	10	US-09-909-320-8	Sequence 8, Appl1	C 952	14.6	0.6	30	9	US-09-426-548-143	Sequence 143, App
C 880	14.8	0.6	49	10	US-09-909-088B-8	Sequence 8, Appl1	C 953	14.6	0.6	30	10	US-09-829-855-152	Sequence 152, App
C 881	14.8	0.6	49	12	US-10-090-624-25	Sequence 25, Appl1	C 954	14.6	0.6	30	10	US-09-797-518A-43	Sequence 43, Appl1
C 882	14.8	0.6	50	9	US-09-905-291A-79	Sequence 79, Appl1	C 955	14.6	0.6	30	10	US-09-231-235-43	Sequence 43, Appl1
C 883	14.8	0.6	50	9	US-09-992-958-144	Sequence 144, App	C 956	14.6	0.6	30	10	US-09-962-035-39	Sequence 39, Appl1
C 884	14.8	0.6	50	9	US-10-029-905-5	Sequence 5, Appl1	C 957	14.6	0.6	30	10	US-09-829-855-148	Sequence 148, App
C 885	14.8	0.6	50	10	US-09-504-231A-2930	Sequence 2930, App	C 958	14.6	0.6	30	10	US-09-829-855-152	Sequence 152, App
C 886	14.8	0.6	50	10	US-09-504-231A-2932	Sequence 2932, App	C 959	14.6	0.6	30	10	US-09-797-518A-44	Sequence 44, Appl1
C 887	14.8	0.6	50	10	US-09-967-013-15	Sequence 15, Appl1	C 960	14.6	0.6	30	10	US-09-797-518A-44	Sequence 44, Appl1
C 888	14.8	0.6	50	10	US-09-967-013-16	Sequence 16, Appl1	C 961	14.6	0.6	30	10	US-09-333-557-17	Sequence 17, Appl1
C 889	14.8	0.6	50	10	US-09-989-722-144	Sequence 144, App	C 962	14.6	0.6	30	10	US-09-804-682-83	Sequence 83, Appl1
C 890	14.8	0.6	50	10	US-09-989-723-144	Sequence 144, App	C 963	14.6	0.6	30	10	US-09-753-352-47	Sequence 47, Appl1
C 891	14.8	0.6	50	10	US-09-989-729-144	Sequence 144, App	C 964	14.6	0.6	30	10	US-09-948-41A-4	Sequence 4, Appl1
C 892	14.8	0.6	50	10	US-09-989-727-144	Sequence 144, App	C 965	14.6	0.6	30	12	US-10-023-529-39	Sequence 39, Appl1
C 893	14.8	0.6	50	10	US-09-274-553D-2930	Sequence 2930, App	C 966	14.6	0.6	30	12	US-10-012-030A-82	Sequence 82, Appl1
C 894	14.8	0.6	50	10	US-09-274-553D-2932	Sequence 2932, App	C 967	14.6	0.6	30	12	US-10-023-523-39	Sequence 39, Appl1
C 895	14.8	0.6	50	10	US-09-734-836-5	Sequence 5, Appl1	C 968	14.6	0.6	31	9	US-09-886-156-25	Sequence 25, Appl1

969 14.6 0.6 31 10 US-09-799-463-9 Sequence 9, Appli
970 14.6 0.6 31 10 US-09-799-994-9 Sequence 9, Appli
971 14.6 0.6 31 10 US-09-801-274-331 Sequence 331, App
972 14.6 0.6 31 10 US-09-801-274-650 Sequence 650, App
973 14.6 0.6 31 10 US-09-801-274-687 Sequence 687, App
974 14.6 0.6 31 10 US-09-801-274-741 Sequence 741, App
975 14.6 0.6 31 10 US-09-801-274-773 Sequence 773, App
976 14.6 0.6 31 10 US-09-801-274-1230 Sequence 1230, Ap
977 14.6 0.6 31 10 US-09-801-274-1358 Sequence 1358, Ap
978 14.6 0.6 31 10 US-09-801-274-1452 Sequence 1452, Ap
979 14.6 0.6 31 10 US-09-801-274-1530 Sequence 1530, Ap
980 14.6 0.6 31 10 US-09-801-274-1599 Sequence 1599, Ap
981 14.6 0.6 31 10 US-09-801-274-1621 Sequence 1621, Ap
982 14.6 0.6 31 10 US-09-801-274-1723 Sequence 1723, Ap
983 14.6 0.6 31 10 US-09-801-274-1776 Sequence 1776, Ap
984 14.6 0.6 31 10 US-09-933-497B-4 Sequence 4, Appli
985 14.6 0.6 32 10 US-09-765-272-374 Sequence 374, App
986 14.6 0.6 32 10 US-09-759-667A-5 Sequence 5, Appli
987 14.6 0.6 32 10 US-09-990-080-7 Sequence 7, Appli
988 14.6 0.6 33 10 US-09-880-006-6 Sequence 6, Appli
989 14.6 0.6 33 10 US-09-759-143-488 Sequence 488, App
990 14.6 0.6 33 10 US-09-780-669-488 Sequence 488, App
991 14.6 0.6 33 10 US-09-950-255-2 Sequence 2, Appli
992 14.6 0.6 33 10 US-09-822-827-488 Sequence 488, App
993 14.6 0.6 33 10 US-09-801-368-20 Sequence 20, Appli
994 14.6 0.6 34 10 US-09-826-212-23 Sequence 23, Appli
995 14.6 0.6 34 10 US-09-784-990-20 Sequence 20, Appli
996 14.6 0.6 34 10 US-09-765-272-321 Sequence 321, App
997 14.6 0.6 35 9 US-09-773-559-13 Sequence 13, Appli
998 14.6 0.6 35 10 US-09-727-311-22 Sequence 22, Appli
999 14.6 0.6 35 10 US-09-746-801A-68 Sequence 68, Appli
1000 14.6 0.6 37 10 US-09-850-799-12 Sequence 12, Appli

ALIGNMENTS

RESULT 1
US-10-108-280-6
; Sequence 6, Application US/10108280
; Patent No. US20020115098A1
; GENERAL INFORMATION:
; APPLICANT: Sosnowski, Ronald G.
; TITLE OF INVENTION: METHODS AND APPARATUS FOR DETERMINATION OF LENGTH
; FILE REFERENCE: DAVID B. MURPHY; Nanogen 256/229
; CURRENT APPLICATION NUMBER: US/10/108,280
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US/09/645,757
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 6
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Human / Biotin
US-10-108-280-6

Query Match 1.0%; Score 22.8; DB 12; Length 49;
Best Local Similarity 79.4%; Pred. No. 1e+04;
Matches 27; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1978 CTCACATTTATTCATTCATTCATTTATTCATT 2011
Db 16 TCATTCATTCATTCATTCATTCATTCATTCATT 49

RESULT 2
US-09-975-408-59/c
; Sequence 59, Application US/09975408
; Patent No. US20020150917A1

; GENERAL INFORMATION:
; APPLICANT: Nanogen, Inc.
; APPLICANT: Weidenhammer, Elaine M.
; APPLICANT: Xu, Xiao
; APPLICANT: Kahl, Brenda F.
; TITLE OF INVENTION: IMPROVED METHODS FOR GENE EXPRESSION MONITORING ON ELECTRONIC
; FILE REFERENCE: 267/174 Patrick S. Bagleman
; CURRENT APPLICATION NUMBER: US/09/975,408
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 09/710,200
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)..(1)
; OTHER INFORMATION: Biotinylated
US-09-975-408-59

Query Match 0.9%; Score 21.8; DB 10; Length 49;
Best Local Similarity 70.7%; Pred. No. 1.8e+04;
Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1979 TCACATTTATTCATTCATTCATTTATTCATTGGGTTGTC 2019

Db 46 TCATTCATTCATTCATTCATTCATTCATTCATTCAGTGGGTTTC 6

RESULT 3
US-10-075-579-59/c
; Sequence 59, Application US/10075579
; Patent No. US20020119484A1
; GENERAL INFORMATION:
; APPLICANT: Nanogen, Inc.
; APPLICANT: Weidenhammer, Elaine M.
; APPLICANT: Wang, Ling
; APPLICANT: Xu, Xiao
; APPLICANT: Heller, Michael J.
; TITLE OF INVENTION: IMPROVED METHODS FOR GENE EXPRESSION MONITORING ON ELECTRONIC
; FILE REFERENCE: 256/262 Patrick S. Bagleman
; CURRENT APPLICATION NUMBER: US/10/075,579
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/710,200
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)..(1)
; OTHER INFORMATION: Biotinylated
US-10-075-579-59

Query Match 0.9%; Score 21.8; DB 12; Length 49;
Best Local Similarity 70.7%; Pred. No. 1.8e+04;
Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1979 TCACATTTATTCATTCATTCATTTATTCATTGGGTTGTC 2019
Db 46 TCATTCATTCATTCATTCATTCATTCATTCATTCAGTGGGTTTC 6

RESULT 4
US-09-920-171-27/c
; Sequence 27, Application US/09920171

RESULT 11
 US-09-944-851-9/C
 ; Sequence 9, Application US/09944851
 ; Patent No. US20020102648A1
 ;
 ; GENERAL INFORMATION:
 ;
 APPLICANT: Alnemrl, Emad S.
 ;
 ; Fernandes-Alnemrl, Teresa
 ; Litwack, Gerald
 ; Armstrong, Robert
 ; Tomaseill, Kevin
 ;
 TITLE OF INVENTION: Mch3, A No. US20020102648A1el Apoptotic Protease
 ;
 ; Nucleic Acids Encoding and Methods of Use
 ;
 NUMBER OF SEQUENCES: 11
 ;
 CORRESPONDENCE ADDRESS:
 ;
 ; ADDRESSEE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/944,851
FILING DATE: 31-Aug-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/556,627
FILING DATE: 13-NOV-1995

ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 1813
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-944-851-9
SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Query Match 0.8%; Score 19.4; DB 10; Length 21;
Best Local Similarity 95.2%; Pred. No. 4.4e+04;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 620 GATGCATCCAGCCGACTCG 640
|||||
Db 21 GATGCATCCAGCCGACTAG 1

RESULT 12
US-09-774-021-17
Sequence 17, Application US/09774021
Patent No. US20020102556A1
GENERAL INFORMATION:
APPLICANT: Laken, Steven J.
APPLICANT: Kinzler, Kenneth W.
APPLICANT: Vogelstein, Bert
TITLE OF INVENTION: Genotyping by Mass Spectrometric Analysis of Short DNA
TITLE OF INVENTION: Fragments
FILE REFERENCE: 01107.73601
CURRENT APPLICATION NUMBER: US/09/774,021
CURRENT FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 09/198,340
PRIOR FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 17
LENGTH: 43
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer for PCR
US-09-774-021-17

Query Match 0.8%; Score 19.4; DB 10; Length 43;
Best Local Similarity 70.3%; Pred. No. 6.3e+04;
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2030 TGTATGTAAACATCTGTTTGGCTTTATGTGCA 2066

|||||
Db 3 TTTATGTATAATTAATCTCTGTGAGATTAATTGCA 39

RESULT 13
US-09-809-905-4/C
Sequence 4, Application US/09809905
Patent No. US2002001806A1
GENERAL INFORMATION:
APPLICANT: Huang, Yuanhui
APPLICANT: Sun, Yi
APPLICANT: Wang, Kevin Ka-Wang
TITLE OF INVENTION: CASPASE-3S SPLICING VARIANT
FILE REFERENCE: U.S. Application A0000224
CURRENT APPLICATION NUMBER: US/09/809,905
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/204,468
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 4
LENGTH: 40
TYPE: DNA
ORGANISM: Homo sapiens
US-09-809-905-4

Query Match 0.8%; Score 19.2; DB 10; Length 40;
Best Local Similarity 75.0%; Pred. No. 6.8e+04;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 925 GCTCACCAAGAACTCTAGTCATATAGC 956
|||||
Db 40 GCTCACAAAGAACTCTATTTATATCATAAC 9

RESULT 14
US-09-944-851-5/C
Sequence 5, Application US/09944851
Patent No. US20020102648A1
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
APPLICANT: Fernandes-Alnemri, Teresa
APPLICANT: Litwack, Gerald
APPLICANT: Armstrong, Robert
APPLICANT: Tomaselli, Kevin
TITLE OF INVENTION: Mch3, A No. US20020102648A1 Apoptotic Protease,
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESS: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/944,851
FILING DATE: 31-Aug-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/556,627
FILING DATE: 13-NOV-1995

ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 1813
TELEPHONE: (619) 535-9001

```
;
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 19 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-944-851-5

Query Match      0.8%; Score 19; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.2e+04;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 701 CTTTCGCTATTCCACGG 719
Db 19 CTTTCGCTATTCCACGG 1

RESULT 15
US-09-884-260A-48
; Sequence 48, Application US/09884260A
; Patent No. US20020098570A1
; GENERAL INFORMATION:
; APPLICANT: Alan Brash
; TITLE OF INVENTION: MUSKELON (CUCUMIS MELO) HYDROPEROXIDE
; FILE REFERENCE: 06027.0002U2
; CURRENT APPLICATION NUMBER: US/09/884,260A
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: 09//,537,357
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: /No. US20020098570A1e -
US-09-884-260A-48

Query Match      0.8%; Score 19; DB 10; Length 46;
Best Local Similarity 71.4%; Pred. No. 8.1e+04;
Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1386 TATTCAGTGTGATTCATTTTCATTCGCTT 1420
Db 9 TAGTGATGTGTGATGATGATGATGATGATGCTT 43

RESULT 16
US-09-284-249-2/C
; Sequence 2, Application US/09284249
; Patent No. US20020155510A1
; GENERAL INFORMATION:
; APPLICANT: Canterbury Health Limited
; APPLICANT: Hart, Derek N J
; TITLE OF INVENTION: Dendritic cell-specific antibodies
; FILE REFERENCE: 24309 MRB
; CURRENT APPLICATION NUMBER: US/09/284,249
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: PCT/NZ97/00134
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: NZ 299537
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 36
; TYPE: DNA
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Made in lab
US-09-284-249-2

Query Match      0.8%; Score 18.6; DB 9; Length 36;
Best Local Similarity 72.7%; Pred. No. 9e+04;
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1775 AGATGGATGAGCTGACGACAGATATAGAGATAC 1807
Db 35 AGAATATACAGACGACGACAGAGTAAGTGAATTC 3

RESULT 17
US-09-867-262-13
; Sequence 13, Application US/09867262
; Patent No. US20020119457A1
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; APPLICANT: FREY, Gerhard
; TITLE OF INVENTION: END SELECTION IN DIRECTED EVOLUTION
; FILE REFERENCE: DEVER1460-17
; CURRENT APPLICATION NUMBER: US/09/867,262
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 09/267,118
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 09/246,178
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: US 09/185,373
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: US 08/760,489
; PRIOR FILING DATE: 1996-12-05
; PRIOR APPLICATION NUMBER: US 60/008,311
; PRIOR FILING DATE: 1995-12-07
; PRIOR APPLICATION NUMBER: US 08/962,504
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: US 08/677,112
; PRIOR FILING DATE: 1996-07-09
; PRIOR APPLICATION NUMBER: US 08/651,568
; PRIOR FILING DATE: 1996-05-22
; PRIOR APPLICATION NUMBER: US 60/008,316
; PRIOR FILING DATE: 1995-12-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Forward primer 9511topF
US-09-867-262-13

QY 1911 AGCAGAGAGAGACAGACAAATGATGTPAAGCC 1943
Db 6 AGGAGAGAGAAATTACATGACGAGCGCTTTAGCC 38

RESULT 18
US-09-885-551A-13
; Sequence 13, Application US/09885551A
; Patent No. US20020146762A1
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; APPLICANT: DUAVERKISHVILI, Tsotne
; APPLICANT: FREY, Gerhard
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED NUCLEIC ACID REASSEMBLY IN
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;; TITLE OF INVENTION: DIRECTED EVOLUTION
;; FILE REFERENCE: DIVER1460-14
;; CURRENT APPLICATION NUMBER: US/09/885,551A
;; CURRENT FILING DATE: 2001-06-19
;; PRIOR APPLICATION NUMBER: US/09/535,754
;; PRIOR FILING DATE: 2000-03-27
;; PRIOR APPLICATION NUMBER: US/09/522,289
;; PRIOR FILING DATE: 2000-03-09
;; NUMBER OF SEQ ID NOS: 14
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 13
;; LENGTH: 39
;; TYPE: DNA
;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: Forward primer 9511topf
US-09-885-551A-13

Query Match 0.8%; Score 18.6; DB 10; Length 39;
Best Local Similarity 72.7%; Pred. No. 9.3e+04;
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 1911 AGCGAGAGAGAACAGAAATGATGATAGCC 1943
Db 6 AGCGAGAGAAATACATGAGCGCTTTAGCC 38

RESULT 19
US-10-087-426-13
; Sequence 13, Application US/10087426
; Patent No. US20020142394A1
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, JAY M.
; TITLE OF INVENTION: EXONUCLEASE-MEDIATED GENE ASSEMBLY IN DIRECTED EVOLUTION
; FILE REFERENCE: DIVER1460-23
; CURRENT APPLICATION NUMBER: US/10/087,426
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/276,860
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/267,118
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 09/246,178
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: US 09/185,373
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: US 08/760,489
; PRIOR FILING DATE: 1996-11-05
; PRIOR APPLICATION NUMBER: US 60/008,311
; PRIOR FILING DATE: 1995-11-07
; PRIOR APPLICATION NUMBER: US 08/962,504
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: US 08/677,112
; PRIOR FILING DATE: 1996-07-09
; PRIOR APPLICATION NUMBER: US 08/651,568
; PRIOR FILING DATE: 1996-05-22
; PRIOR APPLICATION NUMBER: US 60/008,316
; PRIOR FILING DATE: 1995-11-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Forward primer 9511topf
US-10-087-426-13

Query Match 0.8%; Score 18.6; DB 12; Length 39;
Best Local Similarity 72.7%; Pred. No. 9.3e+04;
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 1911 AGCGAGAGAGAACAGAAATGATGATAGCC 1943

Db 6 AGCGAGAGAAATACATGAGCGCTTTAGCC 38

RESULT 20
US-10-108-280-4
; Sequence 4, Application US/10108280
; Patent No. US20020115098A1
; GENERAL INFORMATION:
; APPLICANT: Sosnowski, Ronald G.
; TITLE OF INVENTION: METHODS AND APPARATUS FOR DETERMINATION OF LENGTH
; FILE REFERENCE: POLYMORPHISMS IN DNA
; FILE REFERENCE: DAVID B. MORPHY: Nanogen 256/229
; CURRENT APPLICATION NUMBER: US/10/108,280
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US/09/645,757
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Human / Biotin
US-10-108-280-4

Query Match 0.8%; Score 18.6; DB 12; Length 41;
Best Local Similarity 84.0%; Pred. No. 9.5e+04;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1987 TTATCCATTCATCATTTATTCATT 2011
Db 17 TCATTCATTCATTCATTCATT 41

RESULT 21
US-09-997-956-3
; Sequence 3, Application US/09997956
; Patent No. US20020106714A1
; GENERAL INFORMATION:
; APPLICANT: Jallink, Kees
; TITLE OF INVENTION: Membrane Molecule Indicator Compositions
; FILE REFERENCE: P-NS 5045
; CURRENT APPLICATION NUMBER: US/09/997,956
; CURRENT FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/250,679
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/256,559
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-09-997-956-3

Query Match 0.8%; Score 18.6; DB 10; Length 42;
Best Local Similarity 72.7%; Pred. No. 9.6e+04;
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 26 CTTACCGCGGTGGAGACGATGCGATGATCAG 58
Db 1 CTTGCGCGCGGTACCGATATCAGATGTTGAG 33

RESULT 22
US-09-771-372-1
; Sequence 1, Application US/09771372

Patent No. US20020160361A1
GENERAL INFORMATION:
APPLICANT: LOEHRLEIN, CHRISTINE
APPLICANT: POLIART, DAN
APPLICANT: SHALER, THOMAS
APPLICANT: STEPHENS, KATHY
APPLICANT: TAN, YUPING
APPLICANT: WONG, LINDA
APPLICANT: MONFORTE, JOSEPH
TITLE OF INVENTION: METHODS FOR ANALYSIS OF GENE EXPRESSION
FILE REFERENCE: 14-004510US
CURRENT APPLICATION NUMBER: US/09/771,372
CURRENT FILING DATE: 2001-01-27
PRIOR APPLICATION NUMBER: 60/179,006
PRIOR FILING DATE: 2000-01-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 46
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-771-372-1

Query Match 0.8%; Score 18.4; DB 9; Length 46;
Best Local Similarity 69.4%; Pred. No. 1.1e+05;
Matches 25; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1571 TAGATGATTAAGACAGCAACGACGACGAGAGCTG 1606
DB 10 TATAGATTAACGATACGACCAACCGCAGAGATG 45

RESULT 23
US-09-440-829-14
Sequence 14, Application US/09440829
Patent No. US20020160360A1
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Munishkin, Alexander
APPLICANT: Simonenko, Peter
TITLE OF INVENTION: Long Oligonucleotide Arrays
FILE REFERENCE: C10N015
CURRENT APPLICATION NUMBER: US/09/440,829
CURRENT FILING DATE: 1999-11-15
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 50
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: probe s62_2_50
US-09-440-829-14

Query Match 0.8%; Score 18.4; DB 9; Length 50;
Best Local Similarity 69.4%; Pred. No. 1.2e+05;
Matches 25; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1012 ATTTTATCTCTGTGAATATTCAGAAATTCCTCC 1047
DB 1 ATTCTTGAGAGATCTGGAACCTTCAGATGATGCTCC 36

RESULT 24
US-09-734-836-5/c
Sequence 5, Application US/09734836
Patent No. US20020098475A1
GENERAL INFORMATION:
APPLICANT: No. US20020098475A1artis AG
TITLE OF INVENTION: Bovine Immunodeficiency Virus (BIV) Based Vectors
FILE REFERENCE: 4-30922A

CURRENT APPLICATION NUMBER: US/09/734,836
CURRENT FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: US 09/464,460
PRIOR FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 50
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR primer
NAME/KEY: primer bind
LOCATION: (1)..(50)
US-09-734-836-5

Query Match 0.8%; Score 18.2; DB 10; Length 50;
Best Local Similarity 74.2%; Pred. No. 1.3e+05;
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2224 CTTGATTAATGACTGTTTCTGCTAAT 2254
DB 50 CTTTATTAAGCGCTGTTGCTAAGCATAT 20

RESULT 25
US-09-944-851-8
Sequence 8, Application US/09944851
Patent No. US20020102648A1
GENERAL INFORMATION:
APPLICANT: Alnemri, Emad S.
Alnemri, Teresa
Litwack, Gerald
Armstrong, Robert
Tomasek, Kevin
TITLE OF INVENTION: Mch3, A No. US20020102648A1 Apoptotic Protease,
Nucleic Acids Encoding and Methods of Use
CORRESPONDENCE ADDRESS:
ADDRESS: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/944,851
FILING DATE: 31-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/556,627
FILING DATE: 13-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 1813
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-944-851-8

Query Match 0.8%; Score 18; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 44 ATGGCAGATGATCAGGCG 61
|||||
DB 1 ATGGCAGATGATCAGGCG 18

RESULT 26
US-09-944-851-11/C
; Sequence 11, Application US/09944851
; Patent No. US20020102648A1
; GENERAL INFORMATION:

APPLICANT: Alnemri, Emdad S.
Fernandes-Alnemri, Teresa
Litwack, Gerald
Armstrong, Robert
Tomasselli, Kevin
TITLE OF INVENTION: Mch3, A No. US20020102648A1el Apoptotic Protease,
Nucleic Acids Encoding and Methods of Use
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/944,851
FILING DATE: 31-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/556,627
FILING DATE: 13-NOV-1995

ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 1813
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-944-851-11

Query Match 0.8%; Score 18; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.9e+04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 977 GCTGAGAGCAATGGGTC 994
|||||
DB 18 GCTGAGAGCAATGGGTC 1

RESULT 27
US-09-944-851-10
; Sequence 10, Application US/09944851
; Patent No. US20020102648A1
; GENERAL INFORMATION:
APPLICANT: Alnemri, Emdad S.
Fernandes-Alnemri, Teresa

Litwack, Gerald
Armstrong, Robert
Tomasselli, Kevin
TITLE OF INVENTION: Mch3, A No. US20020102648A1el Apoptotic Protease,
Nucleic Acids Encoding and Methods of Use
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/944,851
FILING DATE: 31-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/556,627
FILING DATE: 13-NOV-1995

ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 1813
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-944-851-10

Query Match 0.8%; Score 18; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 9.6e+04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 638 TCGGGGCCCATCATGAC 655
|||||
DB 4 TCGGGGCCCATCATGAC 21

RESULT 28
US-09-263-959-743/C
; Sequence 743, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:

APPLICANT: Hood, Leroy E.
APPLICANT: Rowen, Lee
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH U
NUMBER OF SEQUENCES: 1279
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

QY 1985 ATTATCCATTCATCATTTATTCATTGGTGT 2018

Db 5 AATTATCAATTAAATTAATTGATTG 33

Oy	1984	AATTATCCAITCAATCATTTATTCATG	2012
Dd	5	AATTATCAATTAAATTAATTATTCATG	33

RESULT 32
US-10-081-281-11/c
; Sequence 11, Application US/10081281
; Patent No. US20020151707A1
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne
; Gross, Jane A.
; Sheppard, Paul
; TITLE OF INVENTION: Immune Mediators and Related Methods
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/081,281
; FILING DATE: 20-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/261,811A
; FILING DATE: 03-Mar-1999
; APPLICATION NUMBER: US 08/480,002
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/482,133
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/483,241
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 60/005,964
; FILING DATE: 27-OCT-1995
; APPLICATION NUMBER: US 08/657,581
; FILING DATE: 07-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Parent, Annette S.
; REGISTRATION NUMBER: 42,058
; REFERENCE/DOCKET NUMBER: 014058-005630US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-081-281-11
Query Match 0.8%; Score 17.8; DB 12; Length 37;
Best Local Similarity 67.6%; Pred. No. 1.4e+05;
Matches 25; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Law, Simon W.
; Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
; BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
; TREATING ATHEROSCLEROSIS
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/962,055
; FILING DATE: 24-Sep-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/979,608
; FILING DATE: 26-NOV-1997
; APPLICATION NUMBER: US 60/031,930
; FILING DATE: 27-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: 10797-002001 (formerly 3983/59818)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...45
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-962-055-30
Query Match 0.8%; Score 17.8; DB 10; Length 45;
Best Local Similarity 62.2%; Pred. No. 1.6e+05;
Matches 28; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

RESULT 34
US-10-023-529-30
; Sequence 30, Application US/10023529.
; Patent No. US20020129388A1
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001
; CURRENT APPLICATION NUMBER: US/10/023,529
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 09/616,289
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/517,849
; PRIOR FILING DATE: 2000-03-02

WANG, MAOLIAN

ABLE OF ANTIGENICITY: SINGLE CHAIN ANTIGEN BINDING PROTEINS CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF

NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:

```

US-09-440-829-26
Query Match          0.8%; Score 17.8; DB 9; Length 50;
Best Local Similarity 75.9%; Pred. No. 1.6e+05;
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1462 AGAAAAGCTTAATGATTCGTGATGTAT 1490
||||| ||||| ||||| ||||| ||
Db 21 AGAAAAGCTTAATGATTCACAAATGTGT 49

RESULT 39
US-09-334-923A-49
; Sequence 49, Application US/09334923A
; Patent No. US20020061551A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Macrophage Inflammatory Protein-4 (MIP-4) Polypeptides (As Amended)
; FILE REFERENCE: 1488.033000D
; CURRENT APPLICATION NUMBER: US/09/334,923A
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 08/208,339
; PRIOR FILING DATE: 1994-03-08
; PRIOR APPLICATION NUMBER: US 08/446,881
; PRIOR FILING DATE: 1995-05-05
; PRIOR APPLICATION NUMBER: US 08/465,682
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/468,775
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/722,719
; PRIOR FILING DATE: 1996-09-30
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA
US-09-334-923A-49

Query Match          0.8%; Score 17.6; DB 10; Length 28;
Best Local Similarity 83.3%; Pred. No. 1.4e+05;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 91 AGCAATGACATTCAGTGCATGC 114
||||| ||||| ||||| ||||| ||
Db 5 AGCTTATGACATTCGTCGCTGC 28

RESULT 40
US-09-334-954A-49
; Sequence 49, Application US/09334954A
; Patent No. US20020076746A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Macrophage Inflammatory Protein-4 (MIP-4) Polynucleotides
; FILE REFERENCE: 1488.033000C
; CURRENT APPLICATION NUMBER: US/09/334,954A
; CURRENT FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: US 08/208,339
; PRIOR FILING DATE: 1994-03-08
; PRIOR APPLICATION NUMBER: US 08/446,881
; PRIOR FILING DATE: 1995-05-05
; PRIOR APPLICATION NUMBER: US 08/465,682
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/468,775
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/722,719
; PRIOR FILING DATE: 1996-09-30

```

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; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 49
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA
US-09-334-954A-49

Query Match
Best Local Similarity 0.8%; Score 17.6; DB 10; Length 28;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 91 AGCAATGACATTCAGTCGATGC 114
Db 5 AGCTATGACATTCGTCGCTGC 28

RESULT 41
US-09-985-442-13/C
; Sequence 13, Application US/09985442
; Patent No. US20020156248A1
; GENERAL INFORMATION:
; APPLICANT: Filpula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: No. US20020156248A1 Method for Targeted Delivery of Nucleic Ac
; FILE REFERENCE: 0977.2300003
; CURRENT APPLICATION NUMBER: US/09/985,442
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/420,592
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide
US-09-985-442-13

Query Match
Best Local Similarity 0.8%; Score 17.6; DB 9; Length 36;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 145 CCTCTTCAGTAGAAGAGAAAA 168
Db 36 CGTCTTCAGTAGAAGAGAAAA 13

RESULT 42
US-09-935-727-40/C
; Sequence 40, Application US/09935727
; Patent No. US20020150583A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
; FILE REFERENCE: PF454P2
; CURRENT APPLICATION NUMBER: US/09/935,727
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/303,224
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/252,131
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/227,598
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: 09/518,931
; PRIOR FILING DATE: 2000-03-03
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; PRIOR APPLICATION NUMBER: 60/168,235
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 60/146,371
; PRIOR FILING DATE: 1999-08-02
; PRIOR APPLICATION NUMBER: 60/131,964
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/131,270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/124,092
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/121,774
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: 09/006,352
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: 60/035,496
; PRIOR FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 40
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Forward TNF-gamma-alpha primer
US-09-935-727-40

Query Match
Best Local Similarity 0.8%; Score 17.6; DB 10; Length 36;
Matches 23; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1179 GATTAATTTCTCTTGTATGTCGTACCTT 1210
Db 35 GATTAATTTCTCATTTGGGAACCTGTAGACTT 4

RESULT 43
US-09-983-580-13/C
; Sequence 13, Application US/09983580
; Patent No. US20020151061A1
; GENERAL INFORMATION:
; APPLICANT: Filpula, David R.
; APPLICANT: Wang, Maoliang
; APPLICANT: Whitlow, Marc D.
; TITLE OF INVENTION: No. US20020151061A1 Method for Targeted Delivery of Nucleic
; FILE REFERENCE: 0977.2300002
; CURRENT APPLICATION NUMBER: US/09/983,580
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/420,592
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/104,949
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
; LENGTH: 36
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide
US-09-983-580-13

Query Match
Best Local Similarity 0.8%; Score 17.6; DB 10; Length 36;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 145 CCTCTTCAGTAGAAGAGAAAA 168
Db 36 CGTCTTCAGTAGAAGAGAAAA 13

RESULT 44
US-09-834-291-18
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Sequence 18, Application US/09834291
Patent No. US20020042064A1
GENERAL INFORMATION:
APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
LENGTH: 40
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-834-291-18

Query Match 0.8%; Score 17.6; DB 10; Length 40;
Best Local Similarity 71.9%; Pred. No. 1.6e+05;
Matches 23; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 558 AACCCCTTTAGAGAAACCAACTCTTC 589
Db 1 AATTAACCTTTAGAGATGCCCAACTGTTTCC 32

RESULT 45
US-09-834-291-26
Sequence 26, Application US/09834291
Patent No. US20020042064A1
GENERAL INFORMATION:
APPLICANT: Krammer, Peter
APPLICANT: Muller-Schilling, Martina
APPLICANT: Oren, Moshe
TITLE OF INVENTION: p53 Binding Areas
FILE REFERENCE: 4121-122
CURRENT APPLICATION NUMBER: US/09/834,291
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/DE99/03343
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: DE 198 47 779.1
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26
LENGTH: 40
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-834-291-26

Query Match 0.8%; Score 17.6; DB 10; Length 40;
Best Local Similarity 71.9%; Pred. No. 1.6e+05;
Matches 23; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 558 AACCCCTTTAGAGAAACCAACTCTTC 589
Db 1 AATTAACCTTTAGAGATGCCCAACTGTTTCC 32

RESULT 46
US-09-238-351-29
Sequence 29, Application US/09238351
Patent No. US20020006643A1
GENERAL INFORMATION:
APPLICANT: Kayem, Jon Paiz
APPLICANT: Banded, Cynthia
TITLE OF INVENTION: Amplification of Nucleic Acids with Electronic
TITLE OF INVENTION: Detection

FILE REFERENCE: A67643/RFT/RMS
CURRENT APPLICATION NUMBER: US/09/238,351
CURRENT FILING DATE: 1999-01-27
EARLIER APPLICATION NUMBER: 09/014,304
EARLIER FILING DATE: 1998-01-27
EARLIER APPLICATION NUMBER: 60/073,011
EARLIER FILING DATE: 1998-01-29
EARLIER APPLICATION NUMBER: 60/084,425
EARLIER FILING DATE: 1998-05-06
EARLIER APPLICATION NUMBER: 60/084,509
EARLIER FILING DATE: 1998-05-06
EARLIER APPLICATION NUMBER: 60/078,102
EARLIER FILING DATE: 1998-03-16
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 29
LENGTH: 41
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-238-351-29

Query Match 0.8%; Score 17.6; DB 10; Length 41;
Best Local Similarity 65.0%; Pred. No. 1.7e+05;
Matches 26; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1179 GATTAATTTCTCTTGTATGTCGTACCTGTGTAATAG 1218
Db 1 GATTACTCTGATGTCGTGTCATCTGTGCATGAGTAG 40

RESULT 47
US-09-737-626A-3/c
Sequence 3, Application US/09737626A
Patent No. US20020144304A1
GENERAL INFORMATION:
APPLICANT: Fincher, Karen
APPLICANT: Plaskinski, Stanislaw
APPLICANT: Wilkinson, Jack
TITLE OF INVENTION: No. US20020144304A1 Plant Expression Constructs
FILE REFERENCE: 38-21(51499)B
CURRENT APPLICATION NUMBER: US/09/737,626A
CURRENT FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: 09/737,626
PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 42
TYPE: DNA
ORGANISM: artificial sequence
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(42)
OTHER INFORMATION: fully synthetic sequence
US-09-737-626A-3

Query Match 0.8%; Score 17.6; DB 10; Length 42;
Best Local Similarity 65.0%; Pred. No. 1.7e+05;
Matches 26; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 152 AGTAAGAAGAAAGAAATGTCACCATGATCCATCAGAGA 191
Db 40 AATATGCAAAAGAAAGAAATGGAAGCTGTATATCAAAAAA 1

RESULT 48
US-10-104-611-18/c
Sequence 18, Application US/10104611
Patent No. US20020160976A1
GENERAL INFORMATION:
APPLICANT: Miles, Vincent J.

Mathews, Michael B.
Katze, Michael G.
Witherell, Gary
Watson, Julia C.
TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
OF VIRAL REPLICATION
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/104,611
FILING DATE: 22-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/221,816B
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7960-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-104-611-18
Query Match 0.8%; Score 17.6; DB 9; Length 45;
Best Local Similarity 65.0%; Pred. No. 1.7e+05;
Matches 26; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
OY 1137 TTATATGTTATTCATTGTCGACTGCTAACTTCTCTT 1176
Db 43 TTTTGATGTCACCTCAGTGAGTATATCTACCTGCTTTT 4
RESULT 49
US-10-112-547-18/c
Sequence 18, Application US/10112547
Patent No. US20020160977A1
GENERAL INFORMATION:
APPLICANT: Miles, Vincent J.
Mathews, Michael B.
Katze, Michael G.
Witherell, Gary
Watson, Julia C.
TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
OF VIRAL REPLICATION
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036/2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/112,547
FILING DATE: 28-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/221,816B
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7960-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-112-547-18
Query Match 0.8%; Score 17.6; DB 9; Length 45;
Best Local Similarity 65.0%; Pred. No. 1.7e+05;
Matches 26; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 1137 TTATATGTTATTCATTGTCGACTGCTAACTTCTCTT 1176
Db 43 TTTTGATGTCACCTCAGTGAGTATATCTACCTGCTTTT 4
RESULT 50
US-09-965-602-27/c
Sequence 27, Application US/09965602
Patent No. US20020103154A1
GENERAL INFORMATION:
APPLICANT: Dimster-Denk, Dago
TITLE OF INVENTION: ESSENTIAL GENES IN YEAST AS TARGETS FOR ANTIUNGAL
TITLE OF INVENTION: AGENTS,
FILE REFERENCE: ACA-8
CURRENT APPLICATION NUMBER: US/09/965,602
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/539,697
PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 27
LENGTH: 45
TYPE: DNA
ORGANISM: primer
US-09-965-602-27
Query Match 0.8%; Score 17.6; DB 10; Length 45;
Best Local Similarity 65.0%; Pred. No. 1.7e+05;
Matches 26; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 2221 ATTCTGATAAATGACTGTTTTCCTGCTAATAGTAC 2260
Db 44 ATTCTGATAAAGTGGGATTTTCTTTTGGCATTTAC 5

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Job time : 144 secs

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OM nucleic - nucleic search, using sw model

Run on: November 10, 2002, 22:35:37 ; Search time 449 Seconds

(without alignments)
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Title: US-09-659-860A-3

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Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 2166140

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 1000 summaries

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24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	2.2	50	22	AA127799
2	39	1.7	50	22	AA127796
3	28	1.2	28	24	ABK67234
4	27.4	1.2	29	22	AA27845
5	27.4	1.2	29	22	AA27846
6	27.4	1.2	29	22	AA27846
7	27.4	1.2	29	22	AA27846
8	27	1.2	27	24	ABN80828
9	27	1.2	27	24	ABK67138

10	26	1.1	26	24	ABN80826	Human caspase 7 fo
11	26	1.1	26	24	ABK67137	Human gene specific
12	26	1.1	26	24	ABK67233	Human gene specific
13	25.6	1.1	48	22	AA013077	Mammalia caspase-3
14	25	1.1	47	21	AA269485	Human map-related
15	24.4	1.1	42	20	AA262544	Caspase-3 PCR prim
16	23.2	1.0	48	18	AA178319	Plasmid vector p2g
17	22.8	1.0	30	18	AA178319	Cysteine protease
18	22.8	1.0	41	18	AAV06633	Transcription enha
19	22	1.0	30	18	AA178319	Cysteine protease
20	22	1.0	50	22	AA130903	Human SNP oligonuc
21	22	1.0	50	22	AA176189	Human silent SNP c
22	21.8	0.9	37	18	AAV06634	Transcription enha
23	21.8	0.9	38	21	AA178319	Plasmid vector p2g
24	21.8	0.9	46	18	AA178319	Plasmid vector p2g
25	21.8	0.9	49	24	ABN17653	Streptococcus agal
26	21.6	0.9	49	18	AA178319	Plasmid vector p2g
27	21.4	0.9	45	22	AA178319	Plasmid vector p2g
28	21.4	0.9	48	22	AA178319	Plasmid vector p2g
29	21.4	0.9	50	22	AA178319	Plasmid vector p2g
30	21.2	0.9	47	22	AA178319	Plasmid vector p2g
31	21.2	0.9	48	22	AA178319	Plasmid vector p2g
32	21	0.9	21	18	AA178319	Plasmid vector p2g
33	21	0.9	33	18	AA178319	Plasmid vector p2g
34	21	0.9	45	18	AA178319	Plasmid vector p2g
35	21	0.9	47	22	AA178319	Plasmid vector p2g
36	21	0.9	47	22	AA178319	Plasmid vector p2g
37	20.8	0.9	41	21	AA178319	Plasmid vector p2g
38	20.8	0.9	41	21	AA178319	Plasmid vector p2g
39	20.8	0.9	41	21	AA178319	Plasmid vector p2g
40	20.8	0.9	48	22	AA178319	Plasmid vector p2g
41	20.8	0.9	48	22	AA178319	Plasmid vector p2g
42	20.8	0.9	49	24	ABN17653	Streptococcus agal
43	20.8	0.9	50	22	AA178319	Plasmid vector p2g
44	20.6	0.9	35	24	ABK66581	Newcastle disease
45	20.6	0.9	35	24	ABK66581	Newcastle disease
46	20.6	0.9	47	21	AA267746	Human map-related
47	20.6	0.9	50	22	AA130421	Human SNP oligonuc
48	20.6	0.9	50	22	AA179057	Human silent SNP c
49	20.6	0.9	50	22	AA179057	Human silent SNP c
50	20.4	0.9	50	22	AA179057	Human silent SNP c
51	20.4	0.9	50	22	AA179057	Human silent SNP c
52	20.4	0.9	50	22	AA179057	Human silent SNP c
53	20.2	0.9	45	24	ABN17171	Streptococcus agal
54	20.2	0.9	47	24	ABN17171	Streptococcus agal
55	20.2	0.9	48	24	ABN17171	Streptococcus agal
56	20.2	0.9	49	13	AA034098	Downstream sequenc
57	20.2	0.9	50	18	AA176878	Staphylococcus aur
58	20.2	0.9	50	20	AA15985	PCR primer B2-3 us
59	20.2	0.9	50	20	AA15985	PCR primer B1-6 us
60	20.2	0.9	50	22	AA130902	Human SNP oligonuc
61	20.2	0.9	50	22	AA179057	Human silent SNP c
62	20.2	0.9	50	22	AA179057	Human silent SNP c
63	20.2	0.9	50	22	AA179057	Human silent SNP c
64	20.2	0.9	50	22	AA179057	Human silent SNP c
65	20	0.9	50	24	ABN17629	Streptococcus agal
66	20	0.9	50	24	ABN17629	Streptococcus agal
67	20	0.9	50	24	ABN17629	Streptococcus agal
68	20	0.9	50	24	ABN17629	Streptococcus agal
69	20	0.9	50	24	ABN17629	Streptococcus agal
70	20	0.9	50	24	ABN17629	Streptococcus agal
71	20	0.9	50	24	ABN17629	Streptococcus agal
72	20	0.9	50	24	ABN17629	Streptococcus agal
73	20	0.9	50	24	ABN17629	Streptococcus agal
74	20	0.9	50	24	ABN17629	Streptococcus agal
75	20	0.9	50	24	ABN17629	Streptococcus agal
76	20	0.9	50	24	ABN17629	Streptococcus agal
77	20	0.9	50	24	ABN17629	Streptococcus agal
78	20	0.9	50	24	ABN17629	Streptococcus agal
79	20	0.9	50	24	ABN17629	Streptococcus agal
80	20	0.9	50	24	ABN17629	Streptococcus agal
81	20	0.9	50	24	ABN17629	Streptococcus agal
82	20	0.9	50	24	ABN17629	Streptococcus agal

C 83	20	0.9	20	24	ABN80859	Human caspase 7 ph	156	19.6	0.8	33	18	AAV06635	Transcription enhan	
C 84	20	0.9	20	24	ABN80860	Human caspase 7 ph	C 157	19.6	0.8	36	22	AAD09368	Toxoplasma gondii	
C 85	20	0.9	20	24	ABN80861	Human caspase 7 ph	C 158	19.6	0.8	37	20	AAAT79805	PCR primer FL5602	
C 86	20	0.9	20	24	ABN80862	Human caspase 7 ph	C 159	19.6	0.8	42	17	AAAT44401	Homology vector 56	
C 87	20	0.9	20	24	ABN80863	Human caspase 7 ph	C 160	19.6	0.8	42	21	AAZ95551	Pseudomonas putida	
C 88	20	0.9	20	24	ABN80864	Human caspase 7 ph	C 161	19.6	0.8	47	21	AAZ68994	Human map-related	
C 89	20	0.9	20	24	ABN80865	Human caspase 7 ph	C 162	19.6	0.8	50	10	AAAN1970	Complementary sequ	
C 90	20	0.9	20	24	ABN80866	Human caspase 7 ph	C 163	19.6	0.8	50	22	AAAL28562	Human SNP oligonuc	
C 91	20	0.9	20	24	ABN80867	Human caspase 7 ph	C 164	19.6	0.8	50	22	AAAL1835	Human SNP oligonuc	
C 92	20	0.9	20	24	ABN80868	Human caspase 7 ph	C 165	19.6	0.8	50	24	ABN71766	Streptococcus agal	
C 93	20	0.9	20	24	ABN80869	Human caspase 7 ph	C 166	19.4	0.8	21	18	AAAT66975	CMH-1 mutagenic PC	
C 94	20	0.9	20	24	ABN80870	Human caspase 7 ph	C 167	19.4	0.8	21	18	AAAT66975	Apoptotic protease	
C 95	20	0.9	20	24	ABN80871	Human caspase 7 ph	C 168	19.4	0.8	38	23	ABK08549	Human CD20 Zinzyme	
C 96	20	0.9	20	24	ABN80872	Human caspase 7 ph	C 169	19.4	0.8	41	19	AAV50525	Brassica sp. polym	
C 97	20	0.9	20	24	ABN80873	Human caspase 7 ph	C 170	19.4	0.8	41	24	ABL16008	Brassica polymorph	
C 98	20	0.9	20	24	ABN80874	Human caspase 7 ph	C 171	19.4	0.8	41	24	ABK12122	Human hrdRI oligon	
C 99	20	0.9	20	24	ABN80875	Human caspase 7 ph	C 172	19.4	0.8	41	24	ABK12123	Human hrdRI oligon	
C 100	20	0.9	20	24	ABN80876	Human caspase 7 ph	C 173	19.4	0.8	43	21	AAAG0141	Human APC gene var	
C 101	20	0.9	20	24	ABN80877	Human caspase 7 ph	C 174	19.4	0.8	46	24	ABO73450	LacZ model system	
C 102	20	0.9	20	24	ABN80878	Human caspase 7 ph	C 175	19.4	0.8	47	21	AAZ65912	Human map-related	
C 103	20	0.9	20	24	ABN80879	Human caspase 7 ph	C 176	19.4	0.8	47	21	AAZ65912	Human map-related	
C 104	20	0.9	20	24	ABN80880	Human caspase 7 ph	C 177	19.4	0.8	47	21	AAZ68315	Human map-related	
C 105	20	0.9	20	24	ABN80881	Human caspase 7 ph	C 178	19.4	0.8	47	21	AAZ68315	RBP-7 biallelic ma	
C 106	20	0.9	20	24	ABN80882	Human caspase 7 ph	C 179	19.4	0.8	50	22	AAI28695	Human SNP oligonuc	
C 107	20	0.9	20	24	ABN80883	Human caspase 7 ph	C 180	19.4	0.8	50	22	AAI28695	Human SNP oligonuc	
C 108	20	0.9	20	24	ABN80884	Human caspase 7 ph	C 181	19.2	0.8	24	24	AAI33536	Human TTP8 specifl	
C 109	20	0.9	20	24	ABN80885	Human caspase 7 ph	C 182	19.2	0.8	24	24	AAI33536	Human TTP8 specifl	
C 110	20	0.9	20	24	ABN80886	Human caspase 7 ph	C 183	19.2	0.8	35	12	AAO11882	Probe NR-2 to arg1	
C 111	20	0.9	20	24	ABN80887	Human caspase 7 ph	C 184	19.2	0.8	35	17	AAAT38491	Primer P5 (HutGM-C	
C 112	20	0.9	20	24	ABN80888	Human caspase 7 ph	C 185	19.2	0.8	36	21	AAAC3888	Human foetal gene	
C 113	20	0.9	20	24	ABN80889	Human caspase 7 ph	C 186	19.2	0.8	36	21	AAAI5855	Primer p5(HutGM-CH	
C 114	20	0.9	20	24	ABN80890	Human caspase 7 ph	C 187	19.2	0.8	38	24	AAI45763	Cancer cells detec	
C 115	20	0.9	20	24	ABN80891	Human caspase 7 ph	C 188	19.2	0.8	40	21	ABLA1740	PCR primer for hum	
C 116	20	0.9	20	24	ABN80892	Human caspase 7 ph	C 189	19.2	0.8	41	24	AAAC4425	Human telomerase (
C 117	20	0.9	20	24	ABN80893	Human caspase 7 ph	C 190	19.2	0.8	42	21	AAAG0462	Murine factor V 3'	
C 118	20	0.9	20	24	ABN80894	Human caspase 7 ph	C 191	19.2	0.8	45	20	AAAX99901	SP6 promoter CS pr	
C 119	20	0.9	20	24	ABN80895	Human caspase 7 ph	C 192	19.2	0.8	46	24	ABN71679	Streptococcus agal	
C 120	20	0.9	20	24	ABN80896	Human caspase 7 ph	C 193	19.2	0.8	47	21	AAZ65862	Human map-related	
C 121	20	0.9	20	24	ABN80897	Human caspase 7 ph	C 194	19.2	0.8	47	21	AAZ65862	Human map-related	
C 122	20	0.9	20	24	ABN80898	Human caspase 7 ph	C 195	19.2	0.8	48	22	AAAT10693	RBS primer used in	
C 123	20	0.9	20	24	ABN80899	Human caspase 7 ph	C 196	19.2	0.8	48	22	AAAT9317	Primer base sequen	
C 124	20	0.9	20	24	ABN80900	Human caspase 7 ph	C 197	19.2	0.8	49	19	AAVA1447	Nucleotide sequen	
C 125	20	0.9	20	24	ABN80901	Human caspase 7 ph	C 198	19.2	0.8	49	22	AAAT98419	Human cDNA clone B	
C 126	20	0.9	20	24	ABN80902	Human caspase 7 ph	C 199	19.2	0.8	50	21	AAZ47149	Liposome membrane-	
C 127	20	0.9	20	24	ABN80903	Human caspase 7 ph	C 200	19.2	0.8	50	22	AAI28332	Human SNP oligonuc	
C 128	20	0.9	20	24	ABN80912	Human caspase 7 ph	C 201	19.2	0.8	50	22	AAI29637	Human SNP oligonuc	
C 129	20	0.9	20	38	24	AAI45271	Human papillomavir	C 202	19.2	0.8	50	22	AAI29637	Hydroxyproline-ric
C 130	20	0.9	20	41	24	ABA92444	Human peroxidase 2	C 203	19.2	0.8	19	18	AAI31687	Human NCO Zinzyme
C 131	20	0.9	20	42	19	AAV57975	Human peroxidase 2	C 204	19.2	0.8	36	24	ABL51734	Human inflammatory
C 132	20	0.9	20	42	21	AAAT7292	Murine PSTIP N-te	C 205	19.2	0.8	38	23	ABK05785	phoA-luc construct
C 133	20	0.9	20	46	13	AAQ27824	Thrombomodulin pro	C 206	19.2	0.8	40	22	AAH91677	Neisseria meningit
C 134	20	0.9	20	49	24	ABN71580	Streptococcus agal	C 207	19.2	0.8	44	20	AAH91677	Primer N5 for nove
C 135	20	0.9	20	49	24	ABN71592	Streptococcus agal	C 208	19.2	0.8	45	21	AAH91677	PCR primer N5, use
C 136	20	0.9	20	50	20	AAK35015	Streptococcus agal	C 209	19.2	0.8	45	21	AAH91677	Newcastle disease
C 137	20	0.9	20	50	22	AAAT5436	Leader oligonucleo	C 210	19.2	0.8	45	22	AAAT5436	PCR primer ocr90 f
C 138	20	0.9	20	50	24	ABK96211	Oligonucleotide us	C 211	19.2	0.8	45	22	AAAT5436	PCR primer ocr90 f
C 139	20	0.9	20	50	24	ABK96211	Respiratory syncyt	C 212	19.2	0.8	46	21	AAH91677	PCR primer for det
C 140	20	0.9	20	50	24	ABK96253	Streptococcus agal	C 213	19.2	0.8	46	21	AAH91677	Muskmelon 9-HPL pa
C 141	20	0.9	20	50	24	ABN71605	Streptococcus agal	C 214	19.2	0.8	46	22	AAH91677	Primer #18. Unde
C 142	20	0.9	20	50	24	ABN71943	Streptococcus agal	C 215	19.2	0.8	46	22	AAH91677	Human map-related
C 143	20	0.9	20	50	24	AAZ55722	Streptococcus agal	C 216	19.2	0.8	46	22	AAH91677	Human map-related
C 144	20	0.9	20	50	24	AAZ37492	Murine caspase-9 R	C 217	19.2	0.8	46	22	AAH91677	Human map-related
C 145	20	0.9	20	50	24	AAZ28213	COX-2 promoter Ets	C 218	19.2	0.8	46	22	AAH91677	Human map-related
C 146	20	0.9	20	50	24	AAZ28282	Mouse splice accep	C 219	19.2	0.8	47	21	AAZ65985	Human map-related
C 147	20	0.9	20	50	24	AAZ38326	Splice acceptor se	C 220	19.2	0.8	47	21	AAZ67432	Human map-related
C 148	20	0.9	20	50	24	AAZ25924	Ceramide affinity	C 221	19.2	0.8	47	21	AAZ65948	Human map-related
C 149	20	0.9	20	50	24	AAZ22909	DE19736591 primer	C 222	19.2	0.8	47	24	ABN71740	Human map-related
C 150	20	0.9	20	50	24	AAZ99389	PCR primer 3'Lac-S	C 223	19.2	0.8	48	20	AAAX30240	Streptococcus agal
C 151	20	0.9	20	50	24	ABN71855	Streptococcus agal	C 224	19.2	0.8	49	20	AAAX80033	PCR amplification
C 152	20	0.9	20	50	24	AAAT62506	Primer for purinoc	C 225	19.2	0.8	49	20	AAAX80034	B. thuringiensis c
C 153	20	0.9	20	50	22	AAAL29270	Human SNP oligonuc	C 226	19.2	0.8	49	21	AAAX08180	B. thuringiensis c
C 154	20	0.9	20	50	22	AAAL29271	Human SNP oligonuc	C 227	19.2	0.8	50	15	AAAX08181	B. thuringiensis c
C 155	20	0.9	20	50	22	AAAL1689	Human SNP oligonuc	C 228	19.2	0.8	50	22	AAAT74372	Capture probe Bb50
	19.8	0.9	50	22	AAAT76477	Human silent SNP c								

229	19	0.8	50	22	AA174720	Human silent SNP c
230	19	0.8	50	22	AA178577	Human silent SNP c
C 231	19	0.8	50	22	AA179055	Human silent SNP c
C 232	19	0.8	50	22	ABN71607	Streptococcus agal
C 233	18.8	0.8	37	20	AAAX91891	Porphyromonas ging
C 234	18.8	0.8	38	16	AAAT54160	Human ICAM hammerh
C 235	18.8	0.8	40	21	AAZ58316	Human peptidase NA
236	18.8	0.8	40	21	AAZ58317	Human peptidase NA
237	18.8	0.8	41	21	AAZ67718	Anti-human VEGF re
238	18.8	0.8	41	21	AAZ70195	Oligonucleotide SE
239	18.8	0.8	42	23	ABL54419	5' flanking region
240	18.8	0.8	42	23	ABL54421	#1 primer identifica
C 241	18.8	0.8	45	21	AAZ87717	Anti-human VEGF re
C 242	18.8	0.8	45	22	AAZ54940	PCR primer used to
C 243	18.8	0.8	45	22	AAZ70194	Oligonucleotide SE
C 244	18.8	0.8	45	22	AAZ82214	Human retrovirus D
C 245	18.8	0.8	46	18	AAZ65781	Repeat sequence fr
C 246	18.8	0.8	46	18	AAZ61263	Major outer membra
C 247	18.8	0.8	47	21	AAZ67480	Human map-related
C 248	18.8	0.8	47	21	AAZ67673	Human map-related
249	18.8	0.8	47	21	AAZ68365	CMS disorder-relat
C 250	18.8	0.8	47	23	AAH88353	Human leukocyte fu
C 251	18.8	0.8	48	15	AAQ69476	Human LFA-1 gene T
252	18.8	0.8	48	18	AAZ63938	Test sequence from
253	18.8	0.8	48	20	AAZ17226	Primer base sequen
C 254	18.8	0.8	48	22	AAZ93310	Primer base sequen
C 255	18.8	0.8	48	22	AAZ93316	DNA binding molecu
C 256	18.8	0.8	48	24	ABK82717	Streptococcus agal
C 257	18.8	0.8	48	24	ABN71594	Primer Forward Lin
C 258	18.8	0.8	50	14	AAQ37397	Trailer MOVHLINK.
C 259	18.8	0.8	50	14	AAQ37416	PCR primer B1-7 us
C 260	18.8	0.8	50	20	AAZ35021	PCR primer B2-2 us
C 261	18.8	0.8	50	20	AAZ15984	Human SNP oligonuc
262	18.8	0.8	50	22	AAZ128051	Human SNP oligonuc
263	18.8	0.8	50	22	AAZ32299	Human SNP oligonuc
264	18.8	0.8	50	22	AAZ34092	Human SNP oligonuc
265	18.8	0.8	50	22	AAZ166209	Vector system rela
266	18.8	0.8	50	22	AAZ174543	Human silent SNP c
267	18.8	0.8	50	22	AAZ178431	Human silent SNP c
C 268	18.8	0.8	50	22	AAH89820	Human coding sequ
C 269	18.8	0.8	50	22	AAZ25442	Oligonucleotide us
C 270	18.8	0.8	50	22	AAZ6217	Respiratory syncyt
C 271	18.8	0.8	50	24	ABK96217	Respiratory syncyt
C 272	18.8	0.8	50	24	ABK96217	Chimpanzee erythro
C 273	18.8	0.8	29	22	AAZ66888	Primer RMW389 for
C 274	18.8	0.8	34	17	AAZ14046	Hunticola insolens
C 275	18.8	0.8	35	17	AAZ13428	PCR primer MK002 u
C 276	18.8	0.8	36	19	AAZ30252	Polynucleotide dir
C 277	18.8	0.8	39	21	AAZ60711	Forward PCR primer
278	18.8	0.8	39	21	AAZ97260	PCR primer 9511top
279	18.8	0.8	39	21	AAZ90020	Esterase gene 5' p
280	18.8	0.8	39	24	AAZ24098	Forward primer, 95
281	18.8	0.8	39	24	AAZ24098	Probe for B. thuri
C 282	18.8	0.8	40	20	AAZ27661	Probe used in clon
C 283	18.8	0.8	40	24	AAZ31620	Phosphatase 9 DNA
284	18.8	0.8	41	22	AAZ48401	Human phospholipas
285	18.8	0.8	42	24	ABK86895	FC-3 common probe
C 286	18.8	0.8	44	24	AAZ17877	Vaccinia virus pro
C 287	18.8	0.8	46	16	AAZ85475	Streptococcus agal
C 288	18.8	0.8	46	24	ABN72388	Human map-related
289	18.8	0.8	47	21	AAZ68269	Human map-related
290	18.8	0.8	47	21	AAZ68269	Genotype assignmen
291	18.8	0.8	48	24	AAZ47414	Synthetic DNA temp
292	18.8	0.8	48	24	ABZ55276	Streptococcus agal
293	18.8	0.8	48	24	ABZ55276	Human interferon a
C 294	18.8	0.8	50	15	AAZ69717	Human interferon a
C 295	18.8	0.8	50	15	AAZ69719	Human interferon a
C 296	18.8	0.8	50	18	AAZ64179	Human interferon l
C 297	18.8	0.8	50	18	AAZ64181	Test sequence from
C 298	18.8	0.8	50	20	AAZ17467	Test sequence from
C 299	18.8	0.8	50	20	AAZ17469	Human SNP oligonuc
C 300	18.8	0.8	50	22	AAZ28094	Human SNP oligonuc
C 301	18.8	0.8	50	22	AAZ28390	Human SNP oligonuc
C 302	18.6	0.8	50	22	AAZ28391	Human SNP oligonuc
C 303	18.6	0.8	50	22	AAZ31689	Human SNP oligonuc
C 304	18.6	0.8	50	22	AAH90372	Human clone c94397
C 305	18.6	0.8	50	24	ABK82958	DNA binding molecu
C 306	18.6	0.8	50	24	ABK82960	DNA binding molecu
C 307	18.6	0.8	50	24	ABN71844	Streptococcus agal
C 308	18.4	0.8	20	24	ABN80928	Mouse caspase 7 ph
C 309	18.4	0.8	20	24	ABN80936	Mouse caspase 7 ph
C 310	18.4	0.8	20	24	ABN80939	Mouse caspase 7 ph
C 311	18.4	0.8	20	24	ABN80940	Mouse caspase 7 ph
C 312	18.4	0.8	20	24	ABN80941	Mouse caspase 7 ph
C 313	18.4	0.8	20	24	ABN80946	Mouse caspase 7 ph
C 314	18.4	0.8	20	24	ABN80959	Mouse caspase 7 ph
C 315	18.4	0.8	26	17	AAZ31579	3' PCR primer for
C 316	18.4	0.8	30	21	AAZ63780	Oligonucleotide fo
C 317	18.4	0.8	40	21	AAZ44466	Dynamic hybridizat
C 318	18.4	0.8	41	22	AAZ30410	Human SNP oligonuc
C 319	18.4	0.8	41	24	AAZ47573	Human hydrogen per
C 320	18.4	0.8	41	24	ABN85083	Human zinc finger
C 321	18.4	0.8	41	24	ABN85083	Human peroxidase 2
C 322	18.4	0.8	44	20	ABZ92445	Microsatellite rep
C 323	18.4	0.8	44	20	ABZ18634	Fat regulated gene
C 324	18.4	0.8	44	24	ABK94873	Human ASTH polymo
C 325	18.4	0.8	46	21	AAZ80541	Streptococcus agal
C 326	18.4	0.8	46	24	ABN71939	PCR primer #4 use
C 327	18.4	0.8	47	21	AAZ65704	Human map-related
C 328	18.4	0.8	47	21	AAZ65704	Human map-related
C 329	18.4	0.8	47	21	AAZ68156	Human map-related
C 330	18.4	0.8	47	21	AAZ68281	Human map-related
C 331	18.4	0.8	47	21	AAZ68977	Human map-related
C 332	18.4	0.8	49	24	ABN71714	Streptococcus agal
C 333	18.4	0.8	49	24	ABN71812	Streptococcus agal
C 334	18.4	0.8	50	22	AAZ3196	HPV probe 20. Syn
C 335	18.4	0.8	50	17	AAZ238175	Human papillomavir
C 336	18.4	0.8	50	17	AAZ29870	Staphylococcus aur
C 337	18.4	0.8	50	20	AAZ68988	Primer P1 used to
C 338	18.4	0.8	50	20	AAZ59747	Human SNP oligonuc
C 339	18.4	0.8	50	22	AAZ131619	Human silent SNP c
C 340	18.4	0.8	50	22	AAZ13196	Human silent SNP c
C 341	18.4	0.8	50	22	AAZ13198	Human silent SNP c
C 342	18.4	0.8	50	22	AAZ175314	Probe oligonucleot
C 343	18.2	0.8	30	22	AAZ77514	Nucleotide sequenc
C 344	18.2	0.8	30	22	AAZ47675	scfv antibody and
C 345	18.2	0.8	32	18	AAZ19543	Recombinant DNA co
C 346	18.2	0.8	32	18	AAZ12950	Primer for chicken
C 347	18.2	0.8	33	18	AAZ88366	Primer 4 relative
C 348	18.2	0.8	33	14	AAZ40389	YXZ construct prim
C 349	18.2	0.8	36	14	AAZ41584	CDNA #4. Unidenti
C 350	18.2	0.8	36	21	AAZ12282	Primer used in con
C 351	18.2	0.8	36	21	AAZ07475	Oligonucleotide us
C 352	18.2	0.8	36	21	AAZ88655	Human TRFP derived
C 353	18.2	0.8	36	21	AAZ88655	PCR primer 2 for t
C 354	18.2	0.8	38	16	AAZ081349	5' oligonucleotide
C 355	18.2	0.8	39	19	AAZ04969	Primer B1AI used
C 356	18.2	0.8	40	19	AAZ05266	Urease gene cyclic
C 357	18.2	0.8	40	21	AAZ13039	bovine respiratory
C 358	18.2	0.8	41	16	AAZ99700	Synthetic oligomer
C 359	18.2	0.8	41	16	AAZ97660	Oligomer DXS17 All
C 360	18.2	0.8	41	18	AAZ97420	Maize polymorphic
C 361	18.2	0.8	41	18	AAZ97420	BRSV strain 375 (V
C 362	18.2	0.8	41	19	AAZ26221	Human basic trans
C 363	18.2	0.8	41	24	AAZ39927	Human-homo autolim
C 364	18.2	0.8	41	24	AAZ99206	Human-homo autolim
C 365	18.2	0.8	41	24	AAZ99207	Chalmydia trachoma
C 366	18.2	0.8	42	10	AAZ92149	Sequence of C. tra
C 367	18.2	0.8	42	10	AAZ97067	Pea praz light-rep
C 368	18.2	0.8	42	21	AAZ97395	Soybean 7S globuli
C 369	18.2	0.8	42	21	AAZ58140	C. trachomatis ser
C 370	18.2	0.8	42	21	AAZ97743	Oligonucleotide co
C 371	18.2	0.8	43	13	AAZ30481	Soluble interleukin
C 372	18.2	0.8	43	17	AAZ32029	3' HUMAN OCR10rc p
C 373	18.2	0.8	43	21	AAZ50753	PCR primer CBL3 fo
C 374	18.2	0.8	43	21	AAZ47510	

C 375	18.2	0.8	43	22	AAH43554	C 448	18	0.8	49	18	AA780517	Hepatoma AS-30D. Ty
C 376	18.2	0.8	44	22	AAH89306	C 449	18	0.8	49	21	AAA37510	Yeast acyltransfer
C 377	18.2	0.8	44	22	AAH89306	C 450	18	0.8	49	21	AAA37510	PCR primer B for G
C 378	18.2	0.8	45	22	AAH84490	C 451	18	0.8	50	14	AAO46276	NE-1 gene exon 4 3
C 379	18.2	0.8	45	22	AAH47672	C 452	18	0.8	50	19	AAH98968	Human EGF-R hairp1
C 380	18.2	0.8	45	24	ABL49540	C 453	18	0.8	50	20	AAH52188	Synthetic plasmid
C 381	18.2	0.8	47	21	AAZ66570	C 454	18	0.8	50	22	AAI28201	Human EGF-R hairp1
C 382	18.2	0.8	47	21	AAZ68001	C 455	18	0.8	50	22	AAI28226	Human SNP oligonuc
C 383	18.2	0.8	47	21	AAZ69037	C 456	18	0.8	50	22	AAI28659	Human SNP oligonuc
C 384	18.2	0.8	47	21	AAZ69040	C 457	18	0.8	50	22	AAI31007	Human SNP oligonuc
C 385	18.2	0.8	48	18	AAZ74743	C 458	18	0.8	50	22	AAI31672	Human SNP oligonuc
C 386	18.2	0.8	48	18	AAZ78649	C 459	18	0.8	50	22	AAI34137	Human SNP oligonuc
C 387	18.2	0.8	48	20	AAZ78649	C 460	18	0.8	50	22	AAI3447	Human SNP oligonuc
C 388	18.2	0.8	48	24	AAZ68511	C 461	18	0.8	50	22	AAI73653	Human silent SNP c
C 389	18.2	0.8	50	19	AAZ68511	C 462	18	0.8	50	22	AAI73653	Human silent SNP c
C 390	18.2	0.8	50	19	AAZ68511	C 463	18	0.8	50	22	AAI73653	Human silent SNP c
C 391	18.2	0.8	50	22	AAZ68511	C 464	18	0.8	50	22	AAI73653	Human silent SNP c
C 392	18.2	0.8	50	22	AAZ68511	C 465	18	0.8	50	22	AAI73653	Human silent SNP c
C 393	18.2	0.8	50	22	AAZ68511	C 466	18	0.8	50	22	AAI73653	Human silent SNP c
C 394	18.2	0.8	50	22	AAZ68511	C 467	18	0.8	50	22	AAI73653	Human silent SNP c
C 395	18.2	0.8	50	22	AAZ68511	C 468	18	0.8	50	22	AAI73653	Human silent SNP c
C 396	18.2	0.8	50	22	AAZ68511	C 469	18	0.8	50	22	AAI73653	Human silent SNP c
C 397	18.2	0.8	50	22	AAZ68511	C 470	18	0.8	50	22	AAI73653	Human silent SNP c
C 398	18.2	0.8	50	22	AAZ68511	C 471	18	0.8	50	22	AAI73653	Human silent SNP c
C 399	18.2	0.8	50	22	AAZ68511	C 472	18	0.8	50	22	AAI73653	Human silent SNP c
C 400	18.2	0.8	50	22	AAZ68511	C 473	18	0.8	50	22	AAI73653	Human silent SNP c
C 401	18	0.8	18	18	AAZ68511	C 474	18	0.8	50	22	AAI73653	Human silent SNP c
C 402	18	0.8	18	18	AAZ68511	C 475	18	0.8	50	22	AAI73653	Human silent SNP c
C 403	18	0.8	18	18	AAZ68511	C 476	18	0.8	50	22	AAI73653	Human silent SNP c
C 404	18	0.8	18	18	AAZ68511	C 477	18	0.8	50	22	AAI73653	Human silent SNP c
C 405	18	0.8	18	18	AAZ68511	C 478	18	0.8	50	22	AAI73653	Human silent SNP c
C 406	18	0.8	18	18	AAZ68511	C 479	18	0.8	50	22	AAI73653	Human silent SNP c
C 407	18	0.8	18	18	AAZ68511	C 480	18	0.8	50	22	AAI73653	Human silent SNP c
C 408	18	0.8	18	18	AAZ68511	C 481	18	0.8	50	22	AAI73653	Human silent SNP c
C 409	18	0.8	18	18	AAZ68511	C 482	18	0.8	50	22	AAI73653	Human silent SNP c
C 410	18	0.8	18	18	AAZ68511	C 483	18	0.8	50	22	AAI73653	Human silent SNP c
C 411	18	0.8	18	18	AAZ68511	C 484	18	0.8	50	22	AAI73653	Human silent SNP c
C 412	18	0.8	18	18	AAZ68511	C 485	18	0.8	50	22	AAI73653	Human silent SNP c
C 413	18	0.8	18	18	AAZ68511	C 486	18	0.8	50	22	AAI73653	Human silent SNP c
C 414	18	0.8	18	18	AAZ68511	C 487	18	0.8	50	22	AAI73653	Human silent SNP c
C 415	18	0.8	18	18	AAZ68511	C 488	18	0.8	50	22	AAI73653	Human silent SNP c
C 416	18	0.8	18	18	AAZ68511	C 489	18	0.8	50	22	AAI73653	Human silent SNP c
C 417	18	0.8	18	18	AAZ68511	C 490	18	0.8	50	22	AAI73653	Human silent SNP c
C 418	18	0.8	18	18	AAZ68511	C 491	18	0.8	50	22	AAI73653	Human silent SNP c
C 419	18	0.8	18	18	AAZ68511	C 492	18	0.8	50	22	AAI73653	Human silent SNP c
C 420	18	0.8	18	18	AAZ68511	C 493	18	0.8	50	22	AAI73653	Human silent SNP c
C 421	18	0.8	18	18	AAZ68511	C 494	18	0.8	50	22	AAI73653	Human silent SNP c
C 422	18	0.8	18	18	AAZ68511	C 495	18	0.8	50	22	AAI73653	Human silent SNP c
C 423	18	0.8	18	18	AAZ68511	C 496	18	0.8	50	22	AAI73653	Human silent SNP c
C 424	18	0.8	18	18	AAZ68511	C 497	18	0.8	50	22	AAI73653	Human silent SNP c
C 425	18	0.8	18	18	AAZ68511	C 498	18	0.8	50	22	AAI73653	Human silent SNP c
C 426	18	0.8	18	18	AAZ68511	C 499	18	0.8	50	22	AAI73653	Human silent SNP c
C 427	18	0.8	18	18	AAZ68511	C 500	18	0.8	50	22	AAI73653	Human silent SNP c
C 428	18	0.8	18	18	AAZ68511	C 501	18	0.8	50	22	AAI73653	Human silent SNP c
C 429	18	0.8	18	18	AAZ68511	C 502	18	0.8	50	22	AAI73653	Human silent SNP c
C 430	18	0.8	18	18	AAZ68511	C 503	18	0.8	50	22	AAI73653	Human silent SNP c
C 431	18	0.8	18	18	AAZ68511	C 504	18	0.8	50	22	AAI73653	Human silent SNP c
C 432	18	0.8	18	18	AAZ68511	C 505	18	0.8	50	22	AAI73653	Human silent SNP c
C 433	18	0.8	18	18	AAZ68511	C 506	18	0.8	50	22	AAI73653	Human silent SNP c
C 434	18	0.8	18	18	AAZ68511	C 507	18	0.8	50	22	AAI73653	Human silent SNP c
C 435	18	0.8	18	18	AAZ68511	C 508	18	0.8	50	22	AAI73653	Human silent SNP c
C 436	18	0.8	18	18	AAZ68511	C 509	18	0.8	50	22	AAI73653	Human silent SNP c
C 437	18	0.8	18	18	AAZ68511	C 510	18	0.8	50	22	AAI73653	Human silent SNP c
C 438	18	0.8	18	18	AAZ68511	C 511	18	0.8	50	22	AAI73653	Human silent SNP c
C 439	18	0.8	18	18	AAZ68511	C 512	18	0.8	50	22	AAI73653	Human silent SNP c
C 440	18	0.8	18	18	AAZ68511	C 513	18	0.8	50	22	AAI73653	Human silent SNP c
C 441	18	0.8	18	18	AAZ68511	C 514	18	0.8	50	22	AAI73653	Human silent SNP c
C 442	18	0.8	18	18	AAZ68511	C 515	18	0.8	50	22	AAI73653	Human silent SNP c
C 443	18	0.8	18	18	AAZ68511	C 516	18	0.8	50	22	AAI73653	Human silent SNP c
C 444	18	0.8	18	18	AAZ68511	C 517	18	0.8	50	22	AAI73653	Human silent SNP c
C 445	18	0.8	18	18	AAZ68511	C 518	18	0.8	50	22	AAI73653	Human silent SNP c
C 446	18	0.8	18	18	AAZ68511	C 519	18	0.8	50	22	AAI73653	Human silent SNP c
C 447	18	0.8	18	18	AAZ68511	C 520	18	0.8	50	22	AAI73653	Human silent SNP c
C 448	18	0.8	18	18	AAZ68511	C 521	18	0.8	50	22	AAI73653	Human silent SNP c
C 449	18	0.8	18	18	AAZ68511	C 522	18	0.8	50	22	AAI73653	Human silent SNP c
C 450	18	0.8	18	18	AAZ68511	C 523	18	0.8	50	22	AAI73653	Human silent SNP c
C 451	18	0.8	18	18	AAZ68511	C 524	18	0.8	50	22	AAI73653	Human silent SNP c
C 452	18	0.8	18	18	AAZ68511	C 525	18	0.8	50	22	AAI73653	Human silent SNP c
C 453	18	0.8	18	18	AAZ68511	C 526	18	0.8	50	22	AAI73653	Human silent SNP c
C 454	18	0.8	18	18	AAZ68511	C 527	18	0.8	50	22	AAI73653	Human silent SNP c
C 455	18	0.8	18	18	AAZ68511	C 528	18	0.8	50	22	AAI73653	Human silent SNP c
C 456	18	0.8	18	18	AAZ68511	C 529	18	0.8	50	22	AAI73653	Human silent SNP c
C 457	18	0.8	18	18	AAZ68511	C 530	18	0.8	50	22	AAI73653	Human silent SNP c
C 458	18	0.8	18	18	AAZ68511	C 531	18	0.8	50	22	AAI73653	Human silent SNP c
C 459	18	0.8	18	18	AAZ68511	C 532	18	0.8	50	22	AAI73653	Human silent SNP c
C 460	18	0.8	18	18	AAZ68511	C 533	18	0.8	50	22	AAI73653	Human silent SNP c
C 461	18	0.8	18	18	AAZ68511	C 534	18	0.8	50	22	AAI73653	Human silent SNP c
C 462	18	0.8	18	18	AAZ68511	C 535	18	0.8	50	22	AAI73653	Human silent SNP c
C 463	18	0.8	18	18	AAZ68511	C 536	18	0.8	50	22	AAI73653	Human silent SNP c
C 464	18	0.8	18	18	AAZ68511	C 537	18	0.8	50	22	AAI73653	Human silent SNP c
C 465	18	0.8	18	18	AAZ68511	C 538	18	0.8	50	22	AAI73653	Human silent SNP c
C 466	18	0.8	18	18	AAZ68511	C 539	18	0.8	50	22	AAI73653	Human silent SNP c
C 467	18	0.8	18	18	AAZ68511	C 540	18	0.8	50	22	AAI73653	Human silent SNP c
C 468	18	0.8	18	18	AAZ68511	C 541	18	0.8	50	22	AAI73653	Human silent SNP c
C 469	18	0.8	18	18	AAZ68511	C 542	18	0.8	50	22	AAI73653	Human silent SNP c
C 470	18	0.8	18	18	AAZ68511	C 543	18	0.8	50	22	AAI73653	Human silent SNP c
C 471	18	0.8	18	18	AAZ68511	C 544	18	0.8	50	22	AAI73653	Human silent SNP c
C 472	18	0.8	18	18	AAZ68511	C 545	18	0.8	50	22	AAI73653	Human silent SNP c
C 473	18	0.8	18	18	AAZ68511	C 546	18	0.8	50	22	AAI73653	Human silent SNP c
C 474	18	0.8	18	18	AAZ68511	C 547	18	0.8	50	22	AAI73653	Human silent SNP c
C 475	18	0.8	18	18	AAZ68511	C 548	18	0.8	50	22	AAI73653	Human silent SNP c
C 476	18	0.8	18	18	AAZ68511	C 549	18	0.8	50	22	AAI73653	Human silent SNP c
C 477	18	0.8	18	18	AAZ68511	C 550	18	0.8	50	22	AAI73653	Human silent SNP c
C 478	18	0.8	18	18	AAZ68511	C 551	18	0.8	50	22	AAI73653	Human silent SNP c
C 479	18	0.8	18	18	AAZ68511	C 552	18	0.8	50	22	AAI73653	Human silent SNP c
C 480	18	0.8	18	18	AAZ68511	C 553	18	0.8	50	22	AAI73653	Human silent SNP c
C 481	18	0.8	18	18	AAZ68511	C 554	18	0.8	50	22	AAI73653	Human silent SNP c
C 482	18	0.8	18	18	AAZ68511	C 555	18	0.8	50	22	AAI73653	Human silent SNP c
C 483	18	0.8	18	18	AAZ68511	C 556	18	0.8	50	22	AAI73653	Human

C 521	17.8	0.8	48	20	AAK17195	Test sequence from	C 594	17.6	0.8	45	14	AA052382	Synthetic template
C 522	17.8	0.8	48	21	AAE89314	HPV 83 ori DNA fra	C 595	17.6	0.8	45	14	AA052393	Sequence used in t
C 523	17.8	0.8	48	24	ABK82686	DNA binding molecu	C 596	17.6	0.8	45	14	AA038288	T7 oligo. Synthet
C 524	17.8	0.8	48	24	ABN71541	Streptococcus agal	C 597	17.6	0.8	45	16	AA035043	Human hippocampal
C 525	17.8	0.8	49	13	AA024354	Oligonucleotide pri	C 598	17.6	0.8	45	17	AA076999	Capping oligonucle
C 526	17.8	0.8	49	19	AAV36530	Self-cleaving G8 D	C 599	17.6	0.8	45	18	AAV00789	5' PCR primer 1a a
C 527	17.8	0.8	49	24	ABN71750	Streptococcus agal	C 600	17.6	0.8	45	18	AAV00744	Capping oligo 1 fo
C 528	17.8	0.8	49	24	ABN71751	Streptococcus agal	C 601	17.6	0.8	45	18	AAV77766	Human FcγRI-gamma
C 529	17.8	0.8	49	24	ABN71987	Streptococcus agal	C 602	17.6	0.8	45	19	AAV14574	Sequence used in c
C 530	17.8	0.8	49	24	ABN72330	Streptococcus agal	C 603	17.6	0.8	45	19	AAV14569	Sequence used in c
C 531	17.8	0.8	50	20	AAK52058	Synthetic plasmid	C 604	17.6	0.8	45	20	AAV79649	HIV RT DNA templat
C 532	17.8	0.8	50	22	AAI28826	Human SNP oligonuc	C 605	17.6	0.8	45	20	AAV79604	T4 DNA polymerase
C 533	17.8	0.8	50	22	AAI28957	Human SNP oligonuc	C 606	17.6	0.8	45	21	AAA28244	Upstream45 primer
C 534	17.8	0.8	50	22	AAI29403	Human SNP oligonuc	C 607	17.6	0.8	45	21	AAA92704	Oligonucleotide #1
C 535	17.8	0.8	50	22	AAI30313	Human SNP oligonuc	C 608	17.6	0.8	45	22	AAA92749	High-affinity nucl
C 536	17.8	0.8	50	22	AAI30422	Human SNP oligonuc	C 609	17.6	0.8	45	22	AAK61080	Influenza virus 5'
C 537	17.8	0.8	50	22	AAI30479	Human SNP oligonuc	C 610	17.6	0.8	45	24	ABK61125	SELEX process nucl
C 538	17.8	0.8	50	22	AAI31739	Human SNP oligonuc	C 611	17.6	0.8	45	24	ABK61125	SELEX process prim
C 539	17.8	0.8	50	22	AAH77526	Probe oligonucleot	C 612	17.6	0.8	46	24	ABK17332	CAMP-dependent pro
C 540	17.8	0.8	50	24	ABN71790	Streptococcus agal	C 613	17.6	0.8	46	22	AAAD09145	Human Cbeta4b and
C 541	17.8	0.8	24	20	AAK31528	Probe for HIV RNA	C 614	17.6	0.8	46	22	AAAD09146	Human Cbeta4b and
C 542	17.6	0.8	24	20	AAK27600	Probe for HIV targ	C 615	17.6	0.8	46	22	AAAD35256	Murine primer #4,
C 543	17.6	0.8	25	18	AAK27600	Primer used in pre	C 616	17.6	0.8	46	24	ABN71621	Streptococcus agal
C 544	17.6	0.8	25	18	AAK27600	Primer used in pre	C 617	17.6	0.8	47	21	AAZ66255	Human map-related
C 545	17.6	0.8	25	22	AAK27600	Murine OPG mutagen	C 618	17.6	0.8	47	21	AAZ66366	Human map-related
C 546	17.6	0.8	26	22	AAK27600	Alfalfa isoflavone	C 619	17.6	0.8	47	21	AAZ66554	Human map-related
C 547	17.6	0.8	26	22	AAK27600	SNP specific upper	C 620	17.6	0.8	47	21	AAZ66688	Human map-related
C 548	17.6	0.8	26	22	AAK27600	Human factor IX (h	C 621	17.6	0.8	47	21	AAZ66873	Human map-related
C 549	17.6	0.8	28	16	AAK27600	Macrophage inflam	C 622	17.6	0.8	47	21	AAZ67472	Human map-related
C 550	17.6	0.8	28	17	AAK27600	Human cytokine Det	C 623	17.6	0.8	47	21	AAZ67476	Human map-related
C 551	17.6	0.8	28	19	AAK27600	Human M-CIF genom	C 624	17.6	0.8	47	21	AAZ67756	Human map-related
C 552	17.6	0.8	28	19	AAK27600	Primer WPF30 for N	C 625	17.6	0.8	47	21	AAZ67833	Human map-related
C 553	17.6	0.8	29	18	AAK27600	Transcription enha	C 626	17.6	0.8	47	21	AAZ68265	Human map-related
C 554	17.6	0.8	32	21	AAK27600	Lobolally pine SSR	C 627	17.6	0.8	47	21	AAZ69185	Human map-related
C 555	17.6	0.8	34	24	ABK51189	Transmissible gast	C 628	17.6	0.8	47	21	AAZ69344	Human map-related
C 556	17.6	0.8	36	24	AAK51189	S100 calcium-bind	C 629	17.6	0.8	47	21	AAK64611	Hepatitis E virus
C 557	17.6	0.8	36	24	AAK51189	Human TNF-gamma-a1	C 630	17.6	0.8	47	21	AAK64611	Sample member clus
C 558	17.6	0.8	36	24	AAK51189	Synthetic oligonuc	C 631	17.6	0.8	47	22	AAK69258	Template YC-100 fo
C 559	17.6	0.8	38	16	AAK51189	Sense primer for h	C 632	17.6	0.8	48	19	AAV63502	M-Raf mitochondria
C 560	17.6	0.8	38	23	ABK05704	Human Chk1 ribozym	C 633	17.6	0.8	48	20	AAZ25262	Fc-VEGF antagonist
C 561	17.6	0.8	38	23	ABK05704	Human NCOG zinzyme	C 634	17.6	0.8	48	21	AAZ69517	RBP-7 biallelic ma
C 562	17.6	0.8	38	23	ABK05704	Human NCOG zinzyme	C 635	17.6	0.8	48	21	AAZ69517	Primer base sequen
C 563	17.6	0.8	38	23	ABK05704	Human NCOG zinzyme	C 636	17.6	0.8	48	22	AAK29313	Metagenic oligo YC
C 564	17.6	0.8	39	14	AAK06563	Human alpha3 (VI)	C 637	17.6	0.8	48	24	AAK29318	Streptococcus agal
C 565	17.6	0.8	39	18	AAK06563	Transcription enha	C 638	17.6	0.8	48	24	ABN71587	Streptococcus agal
C 566	17.6	0.8	40	20	AAK28137	PCR primer for hum	C 639	17.6	0.8	48	24	ABN71587	Streptococcus agal
C 567	17.6	0.8	40	20	AAK28139	PCR primer for hum	C 640	17.6	0.8	48	24	ABN71609	Streptococcus agal
C 568	17.6	0.8	40	21	AAK03169	RSVB polymerase Ia	C 641	17.6	0.8	48	24	ABN71724	Human immunoglobul
C 569	17.6	0.8	40	21	AAK03169	Human MSH6 fragmen	C 642	17.6	0.8	48	24	ABN71724	Oligonucleotide fo
C 570	17.6	0.8	40	22	AAK02686	Human follistatin-	C 643	17.6	0.8	49	17	AAK242957	Synthesized oligon
C 571	17.6	0.8	40	22	AAK02686	Human follistatin-	C 644	17.6	0.8	49	20	AAK242957	PCR primer for the
C 572	17.6	0.8	40	24	ABK99211	Green/red click be	C 645	17.6	0.8	49	21	AAK89784	Synthetic 49-mer o
C 573	17.6	0.8	41	17	AAK28100	Probe OBE2 isolate	C 646	17.6	0.8	49	21	AAK89784	Neuropeptide FF (N
C 574	17.6	0.8	41	19	AAK28100	Maize polymorphic	C 647	17.6	0.8	49	21	AAK294706	Streptococcus agal
C 575	17.6	0.8	41	19	AAK28100	Maize polymorphic	C 648	17.6	0.8	49	24	ABN71866	3', 5' sequence of
C 576	17.6	0.8	41	20	AAK28100	Human sfv library	C 649	17.6	0.8	50	8	AAK70357	ps3 binding site o
C 577	17.6	0.8	41	21	AAK28100	Target probe LP280	C 650	17.6	0.8	50	13	AAK031974	Human c-sis gene,
C 578	17.6	0.8	41	21	AAK28100	Target probe LP280	C 651	17.6	0.8	50	15	AAK031974	Human gene signatu
C 579	17.6	0.8	41	22	AAK28100	LP280 target seque	C 652	17.6	0.8	50	16	AAK23621	Human c-sis gene T
C 580	17.6	0.8	41	22	AAK28100	PCR primer for Dto	C 653	17.6	0.8	50	19	AAK23621	Human c-fos haplpi
C 581	17.6	0.8	41	22	AAK28100	Insulinoid growth	C 654	17.6	0.8	50	19	AAK23621	Potato citrate syn
C 582	17.6	0.8	41	24	ABN86133	Insulinoid growth	C 655	17.6	0.8	50	19	AAK23621	Solandrine glucosy
C 583	17.6	0.8	41	24	ABN86133	Human TFIID subun	C 656	17.6	0.8	50	20	AAK23621	Test sequence from
C 584	17.6	0.8	41	24	ABN86133	Human TFIID subun	C 657	17.6	0.8	50	20	AAK23621	Human clone cg3886
C 585	17.6	0.8	41	24	ABN86133	Oligonucleotide JC	C 658	17.6	0.8	50	21	AAK23621	Arabidopsis thalia
C 586	17.6	0.8	41	24	ABN86133	Oligonucleotide JC	C 659	17.6	0.8	50	21	AAK23621	Lane 1 junction ol
C 587	17.6	0.8	41	24	ABN86133	Human peroxisome I	C 660	17.6	0.8	50	21	AAK23621	Human SNP oligonuc
C 588	17.6	0.8	41	24	ABN86133	Human peroxisome I	C 661	17.6	0.8	50	22	AAK23621	Human SNP oligonuc
C 589	17.6	0.8	42	22	AAK23621	Hepatitis E virus	C 662	17.6	0.8	50	22	AAK23621	Human SNP oligonuc
C 590	17.6	0.8	42	22	AAK23621	Hepatitis E virus	C 663	17.6	0.8	50	22	AAK23621	Human SNP oligonuc
C 591	17.6	0.8	42	22	AAK23621	Arabidopsis thalia	C 664	17.6	0.8	50	22	AAK23621	Human SNP oligonuc
C 592	17.6	0.8	43	19	AAK23621	Tobacco PABP Rsat	C 665	17.6	0.8	50	22	AAK23621	Human SNP oligonuc
C 593	17.6	0.8	43	20	AAK23621	Mouse male enhance	C 666	17.6	0.8	50	22	AAK23621	Human SNP oligonuc

C 667	17.6	0.8	50	22	AAL32445	Human SNP oligonuc	C 740	17.4	0.8	47	24	ABN71571	Streptococcus agal
C 668	17.6	0.8	50	22	AAL34424	Human SNP oligonuc	C 741	17.4	0.8	47	24	ABN71626	Streptococcus agal
C 669	17.6	0.8	50	22	AAL34425	Human SNP oligonuc	C 742	17.4	0.8	47	24	ABN71665	Streptococcus agal
C 670	17.6	0.8	50	22	AAL34550	Human SNP oligonuc	C 743	17.4	0.8	47	24	ABN71710	Streptococcus agal
C 671	17.6	0.8	50	22	AAS43530	Cornedestomatin sin	C 744	17.4	0.8	47	24	ABN71908	Streptococcus agal
C 672	17.6	0.8	50	22	AAI76475	Human silent SNP c	C 745	17.4	0.8	47	24	ABN71908	Streptococcus agal
C 673	17.6	0.8	50	22	AAI76599	Human silent SNP c	C 746	17.4	0.8	50	13	AAO35568	M. jannaschii conu
C 674	17.6	0.8	50	22	AAI77311	Human silent SNP c	C 747	17.4	0.8	50	18	AAV76438	Linker MFSYN276.
C 675	17.6	0.8	50	22	AAI77625	Human silent SNP c	C 748	17.4	0.8	50	19	AAV98891	Staphylococcus aur
C 676	17.6	0.8	50	22	AAH89691	Human synthase cod	C 749	17.4	0.8	50	19	AAV98891	Human EGF-R hairpi
C 677	17.6	0.8	50	24	ABN75034	DNA binding molecu	C 750	17.4	0.8	50	19	AAV68337	Solanidine glucosy
C 679	17.6	0.8	50	24	ABN71608	Human SYCP1 +1 CMN	C 751	17.4	0.8	50	21	AAAC80981	DNA molecule encod
C 680	17.4	0.8	25	21	ABN80916	Human caspase 7 ph	C 752	17.4	0.8	50	21	AAAC80981	Human breast tumo
C 681	17.4	0.8	25	21	AAAC95929	HLA HLA-B gene PCR	C 753	17.4	0.8	50	21	AAAC80981	Oligonucleotide ON
C 682	17.4	0.8	29	20	AAAX29752	Oligo G11top for c	C 754	17.4	0.8	50	21	AAZ65176	Probe specific for
C 683	17.4	0.8	29	22	AAAS44305	Neisseria meningit	C 755	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 684	17.4	0.8	29	22	AAAS44319	N. meningitidis fu	C 756	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 685	17.4	0.8	29	22	AAAD17084	S182 gene mutation	C 757	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 686	17.4	0.8	29	22	AAAT73408	Mouse VEGF PCR for	C 758	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 687	17.4	0.8	30	20	AAAX56441	Oncorhynchus nerka	C 759	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 688	17.4	0.8	30	20	AAAX07403	Bone-stimulatory P	C 760	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 689	17.4	0.8	30	22	AAAC92090	PCR primer #2 used	C 761	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 690	17.4	0.8	33	22	AAAT75914	PCR primer used to	C 762	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 691	17.4	0.8	35	22	AAAC62195	3' primer for huma	C 763	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 693	17.4	0.8	36	14	AAQ46313	P. falciparum gpce	C 764	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 694	17.4	0.8	36	22	AAAT42848	PfEN/MMAC1 DNA mul	C 765	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 695	17.4	0.8	37	21	AAAC82649	Murine PfEN/MMAC1	C 766	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 696	17.4	0.8	37	21	AAAC98630	PfEN/MMAC1 DNA mul	C 767	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 697	17.4	0.8	37	21	AAAC98641	Human ERG G-cleave	C 768	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 698	17.4	0.8	37	21	AAAC98689	Human ERG G-cleave	C 769	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 699	17.4	0.8	37	21	AAAC98689	Human ERG G-cleave	C 770	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 700	17.4	0.8	38	23	ABK05784	Human ERG G-cleave	C 771	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 701	17.4	0.8	38	23	ABK05802	Human ERG G-cleave	C 772	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 702	17.4	0.8	38	23	ABK05956	Human ERG G-cleave	C 773	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 703	17.4	0.8	38	24	ABK08572	Human ERG G-cleave	C 774	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 704	17.4	0.8	39	20	ABK21097	Human ERG G-cleave	C 775	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 705	17.4	0.8	39	20	ABK224697	Human ERG G-cleave	C 776	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 706	17.4	0.8	39	20	ABK224697	Human ERG G-cleave	C 777	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 707	17.4	0.8	40	21	AAZ49144	Human ERG G-cleave	C 778	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 708	17.4	0.8	40	21	AAZ49144	Human ERG G-cleave	C 779	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 709	17.4	0.8	41	21	AAZ49156	Human ERG G-cleave	C 780	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 710	17.4	0.8	41	22	AAAF54056	Human ERG G-cleave	C 781	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 711	17.4	0.8	41	24	ABK51422	Human ERG G-cleave	C 782	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 712	17.4	0.8	41	24	ABK513904	Human ERG G-cleave	C 783	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 713	17.4	0.8	41	24	ABK513904	Human ERG G-cleave	C 784	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 714	17.4	0.8	41	24	ABK513904	Human ERG G-cleave	C 785	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 715	17.4	0.8	42	12	AAQ14326	Human ERG G-cleave	C 786	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 716	17.4	0.8	42	16	AAO86441	Human ERG G-cleave	C 787	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 717	17.4	0.8	42	19	AAV64653	Human ERG G-cleave	C 788	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 718	17.4	0.8	42	19	AAV64653	Human ERG G-cleave	C 789	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 719	17.4	0.8	42	19	AAV64653	Human ERG G-cleave	C 790	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 720	17.4	0.8	44	17	AAAT40242	Human ERG G-cleave	C 791	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 721	17.4	0.8	44	20	AAZ23796	Human ERG G-cleave	C 792	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 722	17.4	0.8	44	21	AAZ23796	Human ERG G-cleave	C 793	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 723	17.4	0.8	44	21	AAZ23796	Human ERG G-cleave	C 794	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 724	17.4	0.8	44	21	AAZ23796	Human ERG G-cleave	C 795	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 725	17.4	0.8	44	24	ABK47015	Human ERG G-cleave	C 796	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 726	17.4	0.8	46	24	ABK47015	Human ERG G-cleave	C 797	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 727	17.4	0.8	46	21	AAAT4924	Human ERG G-cleave	C 798	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 728	17.4	0.8	47	15	AAO72196	Human ERG G-cleave	C 799	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 729	17.4	0.8	47	21	AAZ65727	Human ERG G-cleave	C 800	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 730	17.4	0.8	47	21	AAZ65727	Human ERG G-cleave	C 801	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 731	17.4	0.8	47	21	AAZ65727	Human ERG G-cleave	C 802	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 732	17.4	0.8	47	21	AAZ65727	Human ERG G-cleave	C 803	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 733	17.4	0.8	47	21	AAZ65727	Human ERG G-cleave	C 804	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 734	17.4	0.8	47	21	AAZ65727	Human ERG G-cleave	C 805	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 735	17.4	0.8	47	21	AAZ65727	Human ERG G-cleave	C 806	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 736	17.4	0.8	47	21	AAZ65727	Human ERG G-cleave	C 807	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 737	17.4	0.8	47	21	AAZ65727	Human ERG G-cleave	C 808	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 738	17.4	0.8	47	22	AAZ65727	Human ERG G-cleave	C 809	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
C 739	17.4	0.8	47	23	AAH88387	Human ERG G-cleave	C 810	17.4	0.8	50	22	AAZ65176	Human SNP oligonuc
					AAH88669	CNS disorder-relat	C 811	17.2	0.7	37	21	AAZ65176	Human SNP oligonuc
							C 812	17.2	0.7	37	22	AAH73901	Human SNP oligonuc

813	17.2	0.7	37	24	AA169499	M. utilisima S-hy	c 886	17.2	0.7	47	21	AAZ99608	3' PCR primer used
814	17.2	0.7	38	19	AAV85759	LRP5 exon primer 5	c 887	17.2	0.7	47	22	AA107489	Human reproductiv
815	17.2	0.7	38	19	AAV85837	LRP5 SNP primer 57	c 888	17.2	0.7	47	22	AAE89150	Site-1 protease fu
816	17.2	0.7	38	23	ABK05814	Human MOG0 Zinyme	c 889	17.2	0.7	47	22	AAH20270	PCR primer VHP#3 f
817	17.2	0.7	38	24	ABK21079	Human ERG G-cleave	c 890	17.2	0.7	47	24	ABN71964	Streptococcus agal
818	17.2	0.7	39	12	AAQ11405	Probe COD 1359 spe	c 891	17.2	0.7	47	24	ABK40795	Human obesity-asso
819	17.2	0.7	39	19	AAV21263	Tissue plasminogen	c 892	17.2	0.7	48	17	AAAT4207	Beta-actin gene an
820	17.2	0.7	39	21	AAZ24220	M. thermophila lac	c 893	17.2	0.7	48	21	AAZ55690	HAEPV transfer vec
821	17.2	0.7	39	22	AAH43241	NGC primer #4. Sy	c 894	17.2	0.7	48	22	AAE29298	primer base sequen
822	17.2	0.7	40	20	AAZ20807	Oligonucleotide en	c 895	17.2	0.7	48	22	AAE29299	primer base sequen
823	17.2	0.7	40	20	AAZ67575	PCR primer for S.	c 896	17.2	0.7	48	22	AAE29311	Primer base sequen
824	17.2	0.7	40	20	AAZ76776	Probe for Human DS	c 897	17.2	0.7	48	24	ABN71741	Streptococcus agal
825	17.2	0.7	40	20	AAZ01289	HSP75 sense primer	c 898	17.2	0.7	48	24	ABN71801	Streptococcus agal
826	17.2	0.7	40	21	AAZ94862	Primer 13A used to	c 899	17.2	0.7	49	16	AAO85476	Streptococcus agal
827	17.2	0.7	40	21	AAZ63342	Signalling probe D	c 900	17.2	0.7	49	16	AAO88121	Vaccinia virus pro
828	17.2	0.7	40	21	AAZ40150	Signalling probe D	c 901	17.2	0.7	49	16	AAO88121	Stem-loop oligonuc
829	17.2	0.7	40	22	AAE30176	Nucleoside deoxyri	c 902	17.2	0.7	49	17	AAAT7217	Stem loop oligonuc
830	17.2	0.7	40	24	ABL40580	Sequence of a muta	c 903	17.2	0.7	49	17	AAAT6592	protein antigen b
831	17.2	0.7	41	13	AAO27446	Maize polymorphic	c 904	17.2	0.7	49	17	AAAT6517	PCR primer ZC6302.
832	17.2	0.7	41	19	AAV51085	Maize polymorphic	c 905	17.2	0.7	49	20	AAAI9324	Streptococcus agal
833	17.2	0.7	41	19	AAV47833	Human neurofibroma	c 906	17.2	0.7	49	24	ABN71561	Streptococcus agal
834	17.2	0.7	41	24	ABK51379	Human neurofibroma	c 907	17.2	0.7	49	24	ABN71794	Intergenic region
835	17.2	0.7	41	24	ABK51380	Human ribosomal pr	c 908	17.2	0.7	50	12	AAQ11296	Analyte capture pr
836	17.2	0.7	41	24	ABK99834	Human RalBp1 assoc	c 909	17.2	0.7	50	12	AAQ12942	Analyte capture pr
837	17.2	0.7	41	24	AB199951	Human G protein 10	c 910	17.2	0.7	50	12	AAQ12941	Human MHC class II
838	17.2	0.7	41	24	ABL40240	Human phosphoribos	c 911	17.2	0.7	50	15	AAO69540	Human involucrin m
839	17.2	0.7	41	24	ABL49811	Human insulin-like	c 912	17.2	0.7	50	15	AAO69594	Staphylococcus aur
840	17.2	0.7	41	24	ABA02131	Human insulin-like	c 913	17.2	0.7	50	18	AAV76429	HIV analyte captur
841	17.2	0.7	41	24	ABA02132	Oligonucleotide pr	c 914	17.2	0.7	50	18	AAV74392	HIV analyte captur
842	17.2	0.7	41	24	AAZ20852	PCR primer used to	c 915	17.2	0.7	50	18	AAAT74391	Human involucrin m
843	17.2	0.7	42	21	AAAS9372	T. reesei xylanase	c 916	17.2	0.7	50	18	AAAT64056	Human MHC class II
844	17.2	0.7	42	21	AAA48228	T. reesei xylanase	c 917	17.2	0.7	50	18	AAAT64102	Human complement C
845	17.2	0.7	42	21	AAA48257	C. parvum Cp15/60 P	c 918	17.2	0.7	50	19	AAV71989	Synthetic plasmid
846	17.2	0.7	42	22	AAH45690	Artificial HaEPV D	c 919	17.2	0.7	50	20	AAE21259	Synthetic plasmid
847	17.2	0.7	43	21	AAZ55693	Probe for Human im	c 920	17.2	0.7	50	20	AAE22041	Test sequence from
848	17.2	0.7	43	22	AAZ55698	Artificial HaEPV D	c 921	17.2	0.7	50	20	AAAI7390	Test sequence from
849	17.2	0.7	44	21	AAZ55692	Human oestrogen re	c 922	17.2	0.7	50	20	AAAI7344	PCR primer used to
850	17.2	0.7	44	22	AAI70039	Human oestrogen re	c 923	17.2	0.7	50	21	AAAS4011	E. coli K12 DNAJ o
851	17.2	0.7	44	22	AAH56972	Streptococcus agal	c 924	17.2	0.7	50	21	AAZ98641	Escherichia coli K
852	17.2	0.7	44	22	AAH56973	Human oestrogen re	c 925	17.2	0.7	50	21	AAZ98665	Human SNP oligonuc
853	17.2	0.7	44	22	ABN71865	NRAMP SH3 binding	c 926	17.2	0.7	50	22	AAI30176	Human SNP oligonuc
854	17.2	0.7	45	16	AAO92936	Human lck SH2 doma	c 927	17.2	0.7	50	22	AAI30175	Human SNP oligonuc
855	17.2	0.7	45	17	AAI37297	5' PCR primer for	c 928	17.2	0.7	50	22	AAI30449	Human SNP oligonuc
856	17.2	0.7	45	17	AAI36190	Primer #1 for huma	c 929	17.2	0.7	50	22	AAI30585	Human SNP oligonuc
857	17.2	0.7	45	18	AAE51215	PCR primer for hum	c 930	17.2	0.7	50	22	AAI31544	Human SNP oligonuc
858	17.2	0.7	45	18	AAI68708	Expression vectors	c 931	17.2	0.7	50	22	AAI32219	Human SNP oligonuc
859	17.2	0.7	45	20	AAI78329	Expression vectors	c 932	17.2	0.7	50	22	AAI32385	Human SNP oligonuc
860	17.2	0.7	45	20	AAI78330	HAEPV DNA polymera	c 933	17.2	0.7	50	22	AAI32451	Human SNP oligonuc
861	17.2	0.7	45	21	AAZ55653	Artificial HaEPV D	c 934	17.2	0.7	50	22	AAI32748	Human SNP oligonuc
862	17.2	0.7	45	21	AAZ55691	Library component	c 935	17.2	0.7	50	22	AAI34265	Human SNP oligonuc
863	17.2	0.7	45	22	AAZ59835	Human GDNF gene PC	c 936	17.2	0.7	50	22	AAI34344	Human SNP oligonuc
864	17.2	0.7	46	14	AAO39124	Primer cgt1070 fo	c 937	17.2	0.7	50	22	AAI76775	Human silent SNP c
865	17.2	0.7	46	19	AAV65751	PCR primer used to	c 938	17.2	0.7	50	22	AAI77050	Human G-protein su
866	17.2	0.7	46	22	AAE90066	PCR primer used to	c 939	17.2	0.7	50	22	AAH48693	Human silent nonco
867	17.2	0.7	46	22	AAE55548	Rat FAS CDNA mutag	c 940	17.2	0.7	50	23	ABL00142	Human silent nonco
868	17.2	0.7	46	22	AAE56164	Rat FAS CDNA mutag	c 941	17.2	0.7	50	23	ABL00143	DNA binding molecu
869	17.2	0.7	46	22	AAE56165	Rat FAS CDNA mutag	c 942	17.2	0.7	50	24	ABK82835	DNA binding molecu
870	17.2	0.7	46	22	AAE56166	Streptococcus agal	c 943	17.2	0.7	50	24	ABK82881	Streptococcus agal
871	17.2	0.7	46	24	ABN71733	Phosphatidic acid	c 944	17.2	0.7	50	24	ABN72574	Forward primer for
872	17.2	0.7	47	19	AAV69096	Human map-related	c 945	17	0.7	20	24	ABN83794	Bacteriophage 3A O
873	17.2	0.7	47	21	AAZ66051	Human map-related	c 946	17	0.7	25	21	AAAB68364	Single nucleotide
874	17.2	0.7	47	21	AAZ66803	Human map-related	c 947	17	0.7	27	21	AAAC70348	Single nucleotide
875	17.2	0.7	47	21	AAZ66818	Human map-related	c 948	17	0.7	27	21	AAAC70357	Reverse PCR primer
876	17.2	0.7	47	21	AAZ67051	Human map-related	c 949	17	0.7	27	21	AAA49011	Human 32kDa highly
877	17.2	0.7	47	21	AAZ67147	Human map-related	c 950	17	0.7	27	21	AAH73428	Human chemokine be
878	17.2	0.7	47	21	AAZ67498	Human map-related	c 951	17	0.7	30	19	AAV04485	Human chemokine be
879	17.2	0.7	47	21	AAZ67585	Human map-related	c 952	17	0.7	30	20	AAZ23254	Human lipocalin ho
880	17.2	0.7	47	21	AAZ67938	Human map-related	c 953	17	0.7	30	20	AAAI19510	Human lipocalin ho
881	17.2	0.7	47	21	AAZ67978	Human map-related	c 954	17	0.7	30	21	AAZ94876	Human map-related
882	17.2	0.7	47	21	AAZ68237	Human map-related	c 955	17	0.7	30	22	AAAD16247	Human map-related
883	17.2	0.7	47	21	AAZ68430	Human map-related	c 956	17	0.7	30	22	AAAF77022	Part of bovine der
884	17.2	0.7	47	21	AAZ68664	Human map-related	c 957	17	0.7	30	24	ABL51528	Bovine odorant bin
885	17.2	0.7	47	21	AAZ68732	Human map-related	c 958	17	0.7	30	24	AAAD31069	Human full-length

959	17	0.7	31	20	AAK38961	Human genomic DNA
960	17	0.7	32	18	AAK90574	Primer for CAEV im
961	17	0.7	33	24	ABK11844	Human dihydroxyim
962	17	0.7	34	16	AAK02524	peni gene downstre
963	17	0.7	34	18	AAK64768	Primer Atp Eco/Sp
964	17	0.7	34	19	AAV32357	peni gene downstre
965	17	0.7	34	19	AAV18475	TAT antibody downs
966	17	0.7	34	20	AAK25906	B.licheniformis pe
967	17	0.7	34	21	AAA06164	CFMR gene analysis
968	17	0.7	35	17	AAK31127	Probe Max 277. Sy
969	17	0.7	35	19	AAV27587	Helicobacter pylor
970	17	0.7	35	21	AAZ59523	Hybridisation prob
971	17	0.7	35	22	AAK58535	Cross-linking prob
972	17	0.7	36	17	AAK34758	PCR primer JIA007
973	17	0.7	36	18	AAK86982	Primer used in MHC
974	17	0.7	36	20	AAK15629	Reverse PCR primer
975	17	0.7	36	22	AAK44264	Neisseria meningit
976	17	0.7	36	24	AAK21099	Synthetic oligonuc
977	17	0.7	36	24	ABA01432	Micotiana tabacum
978	17	0.7	37	14	AAQ33350	KHCY cDNA fragment
979	17	0.7	37	15	AAQ73209	Primer PK8978AL to
980	17	0.7	37	19	AAV85646	LRP5 exon primer E
981	17	0.7	37	20	AAK79801	PCR primer FL4529
982	17	0.7	38	13	AAQ35811	HIV-1 gp120 3' reg
983	17	0.7	38	14	AAQ35391	PCR primer HIVM18
984	17	0.7	38	14	AAQ47078	HIV ENV gene PCR p
985	17	0.7	38	17	AAK35819	Primer #8 for prot
986	17	0.7	38	20	AAZ10378	PCR primer used to
987	17	0.7	38	22	AAH96805	Human CHK1 ribozym
988	17	0.7	38	22	AAH96825	Human CHK1 ribozym
989	17	0.7	38	23	ABK05697	Human NOGO zinyme
990	17	0.7	38	23	ABK05791	Human NOGO zinyme
991	17	0.7	38	23	ABK05792	Human NOGO zinyme
992	17	0.7	38	23	ABK05800	Human NOGO zinyme
993	17	0.7	38	23	ABK05873	Human NOGO zinyme
994	17	0.7	38	24	ABK21101	Human ERG G-cleave
995	17	0.7	39	20	AAZ28764	G-less oligonucleo
996	17	0.7	39	21	AAK62594	Human E6-AP lower
997	17	0.7	39	22	AAK91503	Chr gene/PorA prom
998	17	0.7	39	24	AAK47046	Rev-binding sequen
999	17	0.7	39	24	ABK37886	Promoter replaceme
1000	17	0.7	40	19	AAV31611	Nucleotide sequenc

ALIGNMENTS

RESULT 1

AAK27799/c
ID AAK27799 standard; DNA: 50 BP.

AC AAK27799;

DT 24-JAN-2002 (first entry)

DE Human SNP oligonucleotide #1007.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.

OS Homo sapiens.

PN WO200147944-A2.

PD 05-JUL-2001.

PF 28-DEC-2000; 2000WO-US35498.

XX	28-DEC-1999;	99US-0173419.
PR	27-DEC-2000;	2000US-0173419.
XX	(CURA-) CURAGEN CORP.	
PA	Shinkels RA, Leach M;	
PI	WPI; 2001-465210/50.	
DR	Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections	
XX	Claim 1: Page 1667; 4143bp; English.	
XX	The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiotensin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-protein coupled receptors and thioesterases. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic organisms.	
XX	Sequence 50 BP: 20 A; 11 C; 8 G; 11 T; 0 other;	
SO	Query Match 2.2%; Score 50; DB 22; Length 50;	
	Best Local Similarity 100.0%; Pred. No. 0.0042;	
	Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1074 TCAATCAGACAGGAGAACTTCTGCTGCTCTCTCTCTGAAAT 1123	
DB	50 TGATTCACAGGAGGAGAACTTCTGCTGCTCTCTCTCTGAAAT 1	

RESULT 2

AAK27796/c
ID AAK27796 standard; DNA: 50 BP.

AC AAK27796;

DT 24-JAN-2002 (first entry)

DE Human SNP oligonucleotide #1004.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.

OS Homo sapiens.

PN WO200147944-A2.

PD 05-JUL-2001.

PF 28-DEC-2000; 2000WO-US35498.

PR 28-DEC-1999; 99US-0173419.

PF 27-DEC-2000; 2000US-0173419.


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XX PA (CURA-) CURAGEN CORP.
XX PI Shinkets RA, Leach M;
XX DR WPI: 2001-465210/50.
XX PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX PT oncogenes and histones, useful for diagnosing and treating, e.g.
XX PT cancer, autoimmune diseases and infections.
XX PS Claim 1; Page 1667; 4143pp; English.
XX CC The present invention relates to oligonucleotides encoding polymorphic
XX CC variants of proteins related to amylases, amyloid proteins, angiotensin,
XX CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
XX CC histones, kinases, colony stimulating factors, complement related
XX CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
XX CC G-protein coupled receptors and thioesterases. The present sequence is
XX CC one such oligonucleotide. The oligonucleotides and the peptides encoded
XX CC by them may be used in the prevention, diagnosis and treatment of
XX CC diseases associated with inappropriate expression of the proteins listed
XX CC above. Disorders that may be prevented, diagnosed and/or treated include
XX CC multifactorial diseases with a genetic component, such as autoimmune
XX CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
XX CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
XX CC (e.g. cancers of the bladder, brain, breast, colon and kidney/
XX CC leukaemia), diseases of the nervous system and an infection of pathogenic
XX CC organisms.
XX SQ Sequence 50 BP; 10 A; 10 C; 10 G; 20 T; 0 other;

Query Match 1.7%; Score 39; DB 22; Length 50;
Best Local Similarity 98.0%; Pred. No. 2.7;
Matches 50; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1313 GGCAGAAAGATCCCATGTTGACAAACACAGCCAGGGGATATTACT 1363
    |||
DB 50 GGCAGAAAGATCCCATGTTGAC-AAACACAGCCAGGGGATATTACT 1

RESULT 3
ABK67234/C
ID ABK67234 standard; DNA: 28 BP.
XX AC ABK67234;
XX DT 02-JUL-2002 (first entry)
XX DE Human gene specific PCR primer #1322.
XX KM Primer: ss: DNA microarray; differential expression analysis; human.
XX OS Homo sapiens.
XX PN US6352829-B1.
XX PD 05-MAR-2002.
XX PF 05-JAN-1999; 99US-0225928.
XX PR 21-MAY-1997; 97US-0859998.
XX PA (CLON-) CLONTECH LAB INC.
XX PI Chenchik A, Johndaze G, Bibilashvili R;
XX DR WPI: 2002-314699/35.
XX PT Producing sub-population of labeled nucleic acids, useful for analysing
XX PT differences in RNA profiles between several different physiological
XX PT sources, using set of distinct gene specific primers

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PS Example 3; SEQ ID No 1322; 11pp; English.
XX CC The invention relates to producing a sub-population of labeled nucleic
XX CC acids (NAs) comprising contacting a NA sample from a physiological
XX CC source, with a pool of 50 distinct gene specific primers under suitable
XX CC conditions to enzymatically generate sub-population of NAs, where
XX CC each gene specific primer has a sequence complementary to a distinct
XX CC mRNA, and each labeled NA is generated using a single gene specific
XX CC primer. The method is useful for producing a sub-population of labeled
XX CC NAs which is useful for analysing the differences in the RNA profiles
XX CC between several different physiological sources, where the method
XX CC comprises producing subpopulation of labeled NAs for each physiological
XX CC source to identify differences in the population, where the comparison
XX CC is preferably performed by hybridising the labeled NAs for each of the
XX CC distinct physiological sources to an array of probe NAs stably
XX CC associated with the surface of a substrate to produce a hybridisation
XX CC pattern for each of the sources, and comparing the patterns for each of
XX CC the sources, where differential gene expression assays are
XX CC utilised in differential expression analysis of diseased a normal
XX CC tissue e.g. neoplastic a normal tissue, or different tissue or
XX CC subtissue types. The present sequence is a human gene specific PCR
XX CC primer used in the method of the invention.
XX CC Note: The sequence data for this patent did not form part
XX CC of the printed specification, but was obtained in electronic
XX CC format directly from USPTO at
XX CC http.wipo.segdata.uspto.gov/sequence.html?DocID=6352829B1.
XX SQ Sequence 28 BP; 8 A; 5 C; 9 G; 6 T; 0 other;

Query Match 1.2%; Score 28; DB 24; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 859 CTTTGACTCTCAGTCGATGACCCACAC 886
    |||
DB 28 CTTTGACTCTCAGTCGATGACCCACAC 1

RESULT 4
AAF27845
ID AAF27845 standard; DNA: 29 BP.
XX AC AAF27845;
XX DT 02-MAY-2001 (first entry)
XX DE Mutagenic upper primer used to generate human caspase-7 mutant C1865.
XX KM Human; apoptotic; nuclear factor-kappa B; NF-kB; Jun N-terminal kinase;
XX KM JUNK; apoptosis; Caspase-7; caspase-8; mutant; mutagenic primer; ss.
XX OS Homo sapiens.
XX PN US6160095-A.
XX PD 12-DEC-2000.
XX PF 24-AUG-1999; 99US-0382155.
XX PR 07-MAY-1998; 98US-0074044.
XX PA (UNIW ) UNIV WASHINGTON.
XX PA (STOW-) STOWERS INST MEDICAL RES.
XX PI Hood L, Chaudhary PM;
XX DR WPI: 2001-101569/11.
XX PT Novel mutants D73A, L74A and L75A for Caspase 8 useful for regulating
XX PT nuclear factor-kappa B, Jun N-terminal kinase and apoptosis activities,
XX PT for therapeutic purposes

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PS   Disclosure; Column 14; 60pp; English.
XX
XX   The present sequence was used to generate a mutant of a human caspase.
CC   Three novel mutants (D73A, L74A and L75A) for Caspase-8 were also made.
CC   These are useful for regulating NF-kB, JNK and apoptosis activities.
CC   The Caspase-8 mutants are useful for therapeutic purposes and in test
CC   methods or assays for determining whether a candidate compound has a
CC   significant effect upon cell activities, especially NF-kB, JNK and
CC   apoptosis, so as to facilitate the discovery and/or design of therapeutic
CC   agents.
XX
SQ   Sequence 29 BP; 6 A; 8 C; 9 G; 6 T; 0 other;
Query Match      1.2%; Score 27.4; DB 22; Length 29;
Best Local Similarity 96.6%; Pred. No. 2e+03;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY   585 TCTTCATTCAGGCTGCGGAGGACCGAG 613
DB   1 TCTTCATTCAGGCTAGCCGAGGACCGAG 29

RESULT 5
AAF27846/C
XX   AAF27846 standard; DNA; 29 BP.
XX
XX   AAF27846;
XX
XX   02-MAY-2001 (first entry)
XX
XX   Mutagenic lower primer used to generate human caspase-7 mutant C186S.
DE
XX   Human; apoptotic; nuclear factor-kappa B; NF-kB; Jun N-terminal kinase;
KM   JUNK; apoptosis; Caspase-7; caspase-8; mutant; mutagenic primer; ss.
OS   Homo sapiens.
XX
XX   US6160095-A.
XX
XX   12-DEC-2000.
XX
XX   24-AUG-1999; 99US-0382155.
XX
XX   07-MAY-1998; 98US-0074044.
XX
XX   (UNIM ) UNIV WASHINGTON.
PA   (STOW-) STOWERS INST MEDICAL RES.
XX
XX   Hood L, Chaudhary PM;
XX
XX   WPI; 2001-101569/11.
XX
XX   Novel mutants D73A, L74A and L75A for Caspase 8 useful for regulating
PT   nuclear factor-kappa B, Jun N-terminal kinase and apoptosis activities,
PT   for therapeutic purposes -
XX
XX   Disclosure; Column 14; 60pp; English.
XX
XX   The present sequence was used to generate a mutant of a human caspase.
CC   Three novel mutants (D73A, L74A and L75A) for Caspase-8 were also made.
CC   These are useful for regulating NF-kB, JNK and apoptosis activities.
CC   The Caspase-8 mutants are useful for therapeutic purposes and in test
CC   methods or assays for determining whether a candidate compound has a
CC   significant effect upon cell activities, especially NF-kB, JNK and
CC   apoptosis, so as to facilitate the discovery and/or design of therapeutic
CC   agents.
XX
SQ   Sequence 29 BP; 6 A; 9 C; 8 G; 6 T; 0 other;
Query Match      1.2%; Score 27.4; DB 22; Length 29;
Best Local Similarity 96.6%; Pred. No. 2e+03;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY   585 TCTTCATTCAGGCTGCGGAGGACCGAG 613
DB   1 TCTTCATTCAGGCTAGCCGAGGACCGAG 29

RESULT 6
AAF87626
XX   AAF87626 standard; DNA; 29 BP.
XX
XX   AAF87626;
XX
XX   12-JUL-2001 (first entry)
XX
XX   Upper primer for generation of Caspase 7 mutant C186S.
DE
XX   NF-kappaB, JNK; apoptosis; death effector domain; DED; primer; ss.
XX
XX   Homo sapiens.
OS
XX   US6207458-B1.
XX
XX   27-MAR-2001.
XX
XX   07-MAY-1998; 98US-0074044.
XX
XX   07-MAY-1998; 98US-0074044.
XX
XX   07-MAY-1998; 98US-0074044.
XX
XX   (UNIM ) UNIV WASHINGTON.
PA
XX   Chaudhary PM, Hood L;
XX
XX   WPI; 2001-342087/36.
XX
XX   Testing candidate compound affecting cellular NFkappaB JNK, apoptosis
PT   activity by comparing cell activity in presence and absence of
PT   proteinaceous species having two death effector domain and test
PT   compound -
XX
XX   Disclosure; Column 14; 62pp; English.
XX
XX   The present invention relates to testing candidate compounds to
CC   determine whether they affect NF-kappaB, JNK and apoptosis activity.
CC   The method involves the use of 2 death effector domains (DED). The
CC   compounds identified by the invention have therapeutic
CC   applications and are useful for regulating cellular NFkappaB, JNK
CC   and apoptosis activity. The assay is useful for identifying
CC   pharmacological agents or lead compounds generally involved in
CC   assaying for compounds which regulate or modulate a cell activity.
CC   The present sequence is a primer used in the invention.
XX
XX   Sequence 29 BP; 6 A; 8 C; 9 G; 6 T; 0 other;
SQ
Query Match      1.2%; Score 27.4; DB 22; Length 29;
Best Local Similarity 96.6%; Pred. No. 2e+03;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY   585 TCTTCATTCAGGCTGCGGAGGACCGAG 613
DB   1 TCTTCATTCAGGCTAGCCGAGGACCGAG 29

RESULT 7
AAF87627/C
XX   AAF87627 standard; DNA; 29 BP.
XX
XX   AAF87627;
XX
XX   12-JUL-2001 (first entry)
XX
XX   Lower primer for generation of Caspase 7 mutant C186S.
DE
XX   NF-kappaB, JNK; apoptosis; death effector domain; DED; primer; ss.
XX

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OS Homo sapiens.
XX
XX US6207458-B1.
XX
XX 27-MAR-2001.
XX
XX 07-MAY-1998; 98US-0074044.
XX
XX 07-MAY-1998; 98US-0074044.
XX
XX 07-MAY-1998; 98US-0074044.
XX
XX (UNIW ) UNIV WASHINGTON.
XX
XX Chaudhary PM, Hood L;
XX
XX WPI; 2001-342087/36.
XX
XX Testing candidate compound affecting cellular NFkappaB JNK, apoptosis
XX activity by comparing cell activity in presence and absence of
XX PT proteinaceous species having two death effector domain and test
XX compound
XX
XX Disclosure; Column 14; 62pp; English.
XX
XX The present invention relates to testing candidate compounds to
XX determine whether they affect NF-kappaB, JNK and apoptosis activity.
XX The method involves the use of 2 death effector domains (DED). The
XX CC The compounds identified by the invention have therapeutic
XX applications and are useful for regulating cellular NFkappaB, JNK
XX and apoptosis activity. The assay is useful for identifying
XX CC pharmacological agents or lead compounds generally involved in
XX assay for compounds which regulate or modulate a cell activity.
XX The present sequence is a primer used in the invention.
XX
XX Sequence 29 BP; 6 A; 9 C; 8 G; 6 T; 0 other;
SQ
Query Match 1.2%; Score 27.4; DB 22; Length 29;
Best Local Similarity 96.6%; Pred. No. 2e+03;
Matches 28; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 585 TCTTCATTGAGGCTTCCGAGGACCGAG 613
DB 29 TCTTCATTGAGGCTTCCGAGGACCGAG 1
RESULT 8
ABN80828
ID ABN80828 standard; DNA: 27 BP.
XX
XX ABN80828;
XX
XX 15-JUL-2002 (first entry)
XX
XX Human caspase 7 PCR probe SEQ ID NO:6.
XX
XX Caspase 7; antisense modulation; antiinflammatory; cytostatic;
XX KW antisense therapy; caspase 7 inhibitor; inflammatory condition;
XX KW hyperproliferative disorder; cancer; bone metabolism; infection;
XX KW cholesterol disorder; inflammation; tumour; PCR probe; ss.
XX
XX Homo sapiens.
XX
XX WO200222640-A1.
XX
XX 21-MAR-2002.
XX
XX 10-SEP-2001; 2001WO-US28232.
XX
XX 11-SEP-2000; 2000US-0659860.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Zhang H, Watt AT;
XX
XX

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DR WPI; 2002-401902/43.
XX
XX Novel antisense compounds targeted to nucleic acids encoding caspase 7,
XX PT for modulating gene expression and treating diseases associated with
XX PT expression of caspase 7 in humans
XX
XX Example 13; Page 82; 138pp; English.
XX
XX The present invention describes a compound (I) 8-50 nucleobases in
XX length targeted to a nucleic acid molecule encoding caspase 7, which
XX CC specifically hybridises with and inhibits the expression of caspase 7.
XX (I) has antiinflammatory and cytostatic activities, and can be used in
XX CC antisense therapy and as an inhibitor of caspase 7 expression. (I) is
XX CC useful for inhibiting the expression of caspase 7 in human cells or
XX CC tissues, and for treating a human having a disease or condition
XX CC associated with caspase 7 including inflammatory condition,
XX CC hyperproliferative disorder (cancer), or bone metabolism or cholesterol
XX CC disorder. (I) is useful for diagnostics, therapeutics, prophylaxis and
XX CC as research reagent and kits. (I) is useful prophylactically to prevent
XX CC or delay infection, inflammation or tumour formation. The present
XX CC sequence represents a PCR probe for human caspase 7, which is used in
XX CC an example from the present invention.
XX
XX Sequence 27 BP; 10 A; 6 C; 5 G; 6 T; 0 other;
SQ
Query Match 1.2%; Score 27; DB 24; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1305 TTGCACTTGCGCAAAAGAAATCCCAATG 1331
DB 1 TTGCACTTGCGCAAAAGAAATCCCAATG 27
RESULT 9
ABK67138/C
ID ABK67138 standard; DNA: 27 BP.
XX
XX ABK67138;
XX
XX 02-JUL-2002 (first entry)
XX
XX Human gene specific PCR primer #1226.
XX
XX Primer; ss; DNA microarray; differential expression analysis; human.
XX
XX Homo sapiens.
XX
XX US6352829-B1.
XX
XX 05-MAR-2002.
XX
XX 05-JAN-1999; 99US-0225928.
XX
XX 21-MAY-1997; 97US-0859998.
XX
XX (CLON-) CLONTECH LAB INC.
XX
XX Chenchik A, Jokhadze G, Bibilashvili R;
XX
XX WPI; 2002-314699/35.
XX
XX Producing sub-population of labeled nucleic acids, useful for analysing
XX PT differences in RNA profiles between several different physiological
XX PT sources, using set of distinct gene specific primers
XX
XX Example 3; SEQ ID NO 1226; 11pp; English.
XX
XX The invention relates to producing a sub-population of labeled nucleic
XX CC acids (NAs) comprising contacting a NA sample from a physiological
XX CC source, with a pool of 50 distinct gene specific primers under suitable
XX CC conditions to enzymatically generate sub-population of NAs, where
XX CC each gene specific primer has a sequence complementary to a distinct

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CC utilised in differential expression analysis of diseased a normal
 CC tissue e.g. neoplastic a normal tissue, or different tissue or
 CC subltissue types. The present sequence is a human gene specific PCR
 CC primer used in the method of the invention.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from USPTO at
 CC http://wipo.segdata.uspto.gov/sequence.html?DocID=6352829B1.

XX Sequence 26 BP; 7 A; 7 C; 7 G; 5 T; 0 other;
 SQ

Query Match 1.1%; Score 26; DB 24; Length 26;
 Best Local Similarity 100.0%; Pred. No. 4.2e+03;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1605 TGTTCACACACCCAGGCGTATGAGGA 1630
 Db 1 TGTTCACACACCCAGGCGTATGAGGA 26
 |||||||||||||||||||||||||||||

RESULT 12
 ABR67233
 ID ABR67233 standard; DNA; 26 BP.
 XX ABR67233;
 AC ABR67233;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Human gene specific PCR primer #1321.
 KW Primer; ss; DNA microarray; differential expression analysis; human.
 XX
 OS Homo sapiens.
 XX
 PN US6352829-B1.
 PD 05-MAR-2002.
 XX
 PE 05-JAN-1999; 99US-0225928.
 XX
 PR 21-MAY-1997; 97US-0859998.
 XX
 PA (CLON-) CLONTECH LAB INC.
 PI Chenchik A, Jokhadze G, Biblilashvili R;
 DR WPI; 2002-314699/35.
 XX
 XX Producing sub-population of labeled nucleic acids, useful for analysing
 PT differences in RNA profiles between several different physiological
 PT sources, using set of distinct gene specific primers -
 PT
 XX Example 3; SEQ ID No 1321; 11pp; English.

XX The invention relates to producing a sub-population of labeled nucleic
 CC acids (NAs) comprising contacting a NA sample from a physiological
 CC source, with a pool of 50 distinct gene specific primers under suitable
 CC conditions to enzymatically generate sub-population of NAs, where
 CC each gene specific primer has a sequence complementary to a distinct
 CC mRNA, and each labeled NA is generated using a single gene specific
 CC primer. The method is useful for producing a sub-population of labeled
 CC NAs which is useful for analysing the differences in the RNA profiles
 CC between several different physiological sources, where the method
 CC comprises producing subpopulation of labeled NAs for the different
 CC physiological sources, comprising the populations for each physiological
 CC source to identify differences in the population, where the comparison
 CC is preferably performed by hybridising the labeled NAs for each of the
 CC distinct physiological sources to an array of probe NAs stably
 CC associated with the surface of a substrate to produce a hybridisation
 CC pattern for each of the sources, and comparing the patterns for each of
 CC the sources, where differential gene expression assays are
 CC utilised in differential expression analysis of diseased a normal
 CC tissue e.g. neoplastic a normal tissue, or different tissue or

CC subltissue types. The present sequence is a human gene specific PCR
 CC primer used in the method of the invention.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from USPTO at
 CC http://wipo.segdata.uspto.gov/sequence.html?DocID=6352829B1.

XX Sequence 26 BP; 4 A; 7 C; 7 G; 8 T; 0 other;
 SQ

Query Match 1.1%; Score 26; DB 24; Length 26;
 Best Local Similarity 100.0%; Pred. No. 4.2e+03;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 584 TTCTTCATTCAGCGCTTGCCGAGGAC 609
 Db 1 TTCTTCATTCAGCGCTTGCCGAGGAC 26
 |||||||||||||||||||||||||||||

RESULT 13
 AAD13077/C
 ID AAD13077 standard; DNA; 48 BP.
 XX AAD13077;
 AC AAD13077;
 XX
 DT 16-OCT-2001 (first entry)
 XX
 DE Mammalia caspase-3 cDNA amplifying PCR primer, C33.
 XX
 KW Protein destabilisation; linker moiety; reporter moiety; disease model;
 KW linear multimerised domain; -NH-ubiquitin protein endoprotease;
 KW transgenic animal; transgenic plant; disease resistance;
 KW caspase-3; PCR primer; ss.
 XX
 OS Mammalia.
 XX
 PN WO200157242-A2.
 PD 09-AUG-2001.
 XX
 PE 02-FEB-2001; 2001WO-US03791.
 XX
 PR 04-FEB-2000; 2000US-0498098.
 XX
 PA (AURO-) AURORA BIOSCIENCES CORP.
 PI Stack JH, Whitney M, Cubitt AB, Pollock BA;
 DR WPI; 2001-488890/53.
 XX
 XX Destabilizing proteins in living cells, by coupling a target protein to
 PT linear multimerized destabilization domain non-cleavable by
 PT -NH-ubiquitin protein endoproteases, comprising two copies of the
 PT domain -
 PT
 XX Example 4; Page 132; 171pp; English.

XX The present invention relates to a method for destabilising a target
 CC protein in a cell. The method comprises a linker moiety which operatively
 CC couples a target protein (a reporter moiety) to a linear multimerised
 CC destabilising domain, which is non-cleavable by a -NH-ubiquitin protein
 CC endoproteases. The method is useful for detecting an activity such as
 CC protease, protein kinase or phosphoprotein phosphatase activity and is
 CC also useful for identifying modulators of these activities. The method
 CC is also useful for developing novel assays for a wide range of
 CC post-translational activities, such as proteolysis, phosphorylation,
 CC dephosphorylation, glycosylation, methylation, sulfation, prenylation,
 CC disulfide bond formation and APP-ribosylation within cells. The
 CC recombinant DNA molecule of the invention is useful for creating
 CC transgenic animals useful as disease models and transgenic plants with
 CC improved disease resistance or other favourable traits. The present
 CC sequence is a PCR primer which is used for the amplification of mammaia
 CC caspase-3 cDNA, used as a reporter moiety in the exemplification of
 CC the invention.

```

Query Match          1.1%; Score 25; DB 21; Length 47;
Best Local Similarity 75.6%; Pred. No. 1e+04;
Matches    31; Conservative    0; Mismatches   10; Indels     0; Gaps      0

QY      1504 GTCTGGAACAGAACCATTCATGTAGTGGTTCCAAACAGAGG 1544
         ||||||| ||||| ||||| ||||| ||||| ||||| |||||
Db       4 GTGAGGAACAGCAAAACACGCTAGTATTTCAAAACAAGTG 44

RESULT 15
ID      AA225254 standard; DNA; 42 BP.
AA225254
XX      AA225254;
AC
XX
DT      15-DEC-1999 (first entry)
XX
DE      Caspase-3 PCR primer SEQ ID NO:10.
XX
KW      Apoptosis; regulation; chemically induced dimerisation; aggregation;
KM      artificial death switch; AD5; cysteine protease; caspase-1; ICE;
KM      caspase-3; YAMA; FK506-binding protein; FKBP; development;
KM      hyperproliferative disorder; tumour; PCR primer; ss.
XX
OS      Synthetic.
XX
PN      WO950425-A2.
PD
PI      07-OCT-1999.
PF      30-MAR-1999; 99WO-US06799.
PR      30-MAR-1998; 98US-0079831.
PA      (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
PI      Spencer DM, Slawin KM;
XX
DR      WPI; 1999-591323/50.
XX
PT      Conditionally lethal artificial death switches based on chemically
PT      induced dimerisation of cysteine proteases - useful for treating
PT      hyperproliferative diseases
XX
PS      Example 1; Page 20; 117pp; English.
XX
CC      The present invention describes a conditionally lethal molecule (A)
CC      comprising a chemical inducer binding domain and an apoptosis inducing
CC      factor, where the apoptosis inducing factor is an apoptosis signal
CC      transducing factor. A vector encoding (A) is useful for treating a
CC      disease, e.g. a hyperproliferative disease that is benign or malignant,
CC      or arteriosclerosis. The nucleotide sequence (I) encoding (A) can be
CC      used to cause regression of a tumour, reduction in tumour size or
CC      reduction in PSA levels, by transfecting the nucleic acid into cells of
CC      the tumour. (I) can also be used to affect the rate of cell proliferation
CC      caused by BPH by transfecting (I) into prostate cells. (I) is also used
CC      to induce apoptosis in a cell as well as for determining the biological
CC      role of a cell type. The conditionally lethal gene is non-toxic unless
CC      induced. It does not require membrane localisation and bypasses
CC      endogenous apoptosis control mechanisms. The present sequence represents
CC      a PCR primer used in an example from the present invention.
XX
SQ      Sequence 42 BP; 8 A; 11 C; 13 G; 10 T; 0 other;

Query Match          1.1%; Score 24.4; DB 20; Length 42;
Best Local Similarity 73.8%; Pred. No. 1.4e+04;
Matches    31; Conservative    0; Mismatches   11; Indels     0; Gaps      0;

QY      590 ATTCAAGGCTTCGCAGGAGCAGCGATTGATGATGCAATCCAG 631
         ||||||| ||||| ||||| ||||| ||||| ||||| |||||
Db       1 ATTCAAGGCTTCGCCGTGTAACGAACTGCACTGTGCATTGAG 42

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PD 30-OCT-1997.
 XX
 PF 10-APR-1997; 97WO-FR00636.
 XX
 PR 25-APR-1996; 96FR-0005223.
 XX
 PA (RHON) RHONE-POULENC RORER SA.
 XX
 PI Mallet J, Meloni R, Ravassard P, Trelhou F;
 XX WPI: 1997-549358/50.
 DR
 XX
 PT Transcription enhancers derived from first intron of tyrosine
 PT hydroxylase gene - useful in expression vectors for producing
 PT proteins especially for gene therapy
 XX
 PS Claim 6; Page 21; 42pp; French.

CC This sequence represents a specifically claimed DNA fragment derived
 CC from the first intron of the tyrosine hydroxylase gene containing an
 CC allele of the HUMTHOI microsatellite. The invention relates to a new
 CC isolated DNA fragment (A) which has transcription enhancing activity and
 CC is defined as: (a) consisting of part of the first intron of the
 CC tyrosine hydroxylase (TH) gene, especially an allele of the HUMTHOI
 CC microsatellite; or (b) possessing the sequence (1): (TCAT)n-(CAT)o-
 CC (TCAT)p (1) n = 1-50; o = 0-20; and p = 0-50. The new enhancers are
 CC incorporated into expression cassettes and plasmid or viral vectors for
 CC expressing proteins in vitro, in vivo or ex vivo. They are especially
 CC intended for use in mammalian cells for gene therapy, e.g. of cancer or
 CC restenosis.

XX Sequence 41 BP; 9 A; 14 C; 0 G; 18 T; 0 other;

Query Match 1.0%; Score 22.8; DB 18; Length 41;
 Best Local Similarity 79.4%; Pred. No. 3.5e+04;
 Matches 27; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 1978 CTCACAAATTATCCATTCATTCATTTATTCATT 2011
 DB 3 CTCATTCATTCATTCATTCATTCATTCATTCATT 36

RESULT 19
 AAT66978/C
 ID AAT66978 standard; DNA; 30 BP.
 XX
 AC AAT66978;
 XX

DT 21-JUL-1997 (first entry)

XX Cysteine protease CMH-1 PCR primer.

XX Cysteine protease; CMH-1; CPP32/Mch2 homologue-1; apoptosis;
 KW programmed cell death; cancer; neurodegenerative disease;
 KW autoimmune disease; gene therapy; diagnosis; primer; PCR;
 KW polymerase chain reaction; ss.

XX Synthetic.

OS W09716552-A1.

XX W09716552-A1.

XX 09-MAY-1997.

XX 01-NOV-1996; 96WO-US17431.

XX 16-NOV-1995; 95US-0558733.

XX 03-NOV-1995; 95US-0007211.

XX 06-NOV-1995; 95US-0007251.

XX (VERT-) VERTEX PHARM INC.

XX Lipkpe JA, Su M;

DR WPI: 1997-272121/24.

XX
 XX DNA encoding active, activatable or inactive cysteine protease CMH-1
 PT - useful in gene therapy for promoting and inhibiting apoptosis and
 PT for diagnosing cells with potential for apoptosis
 XX

PS Example 3; Page 25; 48pp; English.

XX PCR primers (AAT66977-78) were designed to introduce in-frame XhoI
 CC sites to the 5' and 3' ends of human cysteine protease cmh-1
 CC cDNA (see also AAT66970). The PCR product XhoI fragment was ligated
 CC into pET-15b inducible E. coli expression vector. The resulting
 CC plasmid encoded a polypeptide comprising a 23-residue N-terminal
 CC peptide (AAW15248) contg. a hexahistidine tag and thrombin cleavage
 CC site, fused to Ala24 of CMH-1. Hexahistidine-tagged CMH-1 (Ala24-
 CC Gln303) was produced in E. coli BM21 (DE3) transformants.

XX Sequence 30 BP; 7 A; 5 C; 10 G; 8 T; 0 other;

Query Match 1.0%; Score 22; DB 18; Length 30;
 Best Local Similarity 100.0%; Pred. No. 4.8e+04;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 935 GAACCTACTCTCAGTCATATAGC 956
 DB 30 GAACCTACTCTCAGTCATATAGC 9

RESULT 20

AAL30903/C
 ID AAL30903 standard; DNA; 50 BP.

XX AAL30903;

DT 24-JAN-2002 (first entry)

XX Human SNP oligonucleotide #4111.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neutrotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinase; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease; ss.

XX Homo sapiens.

XX W0200147944-A2.

XX 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US35498.

XX 28-DEC-1999; 99US-0173419.

XX 27-DEC-2000; 2000US-0173419.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

XX WPI: 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -
 XX
 PS Claim 1; Page 2567; 4143pp; English.

XX The present invention relates to oligonucleotides encoding polymorphic
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,

CC complementary sequences may also be used as DNA probes in diagnostic

Best Local SIM:
Matches 26:

Query Match	0.9%;	Score 21.8;	DB 18;	Length 37;
Best Local Similarity	78.8%;	Pred. No. 6e+04;		
Matches	26;	Conservative	0;	Mismatches 7;
			Indels	0;
			Gaps	0;

OY 1978 CTCACAAATTATTCATTCATTTATTCAT 2010
 |||| |||| |||| |||| ||||
 Db 3 CTCATTCATTCATTCATTCATTCATTCAT 35

RESULT 23 AAC62133/C

ID AAC62133 standard; DNA; 38 BP.

AC AAC62133;

DT 06-MAR-2001 (first entry)

DE Primer used to amplify the right end of the BAV-1 genome.

XX Early gene region; E3; E4; vaccine; bovine adenovirus type 1; BAV-1;
 KW gene therapy; PCR primer; ss.

OS Mastadenovirus host.

PN WO200061773-A1.

PD 19-OCT-2000.

PF 07-APR-2000; 2000WO-US09459.

PR 09-APR-1999; 99US-0289930.

PA (SCHE) SCHERING-PLOUGH LTD.

PI Chiang CH, Cochran MD;

DR WPI; 2000-656327/63.

PT Recombinant and mutant viruses derived from bovine adenovirus useful
 for generating vaccines that induce an immune response in animals

PS Disclosure; Page 19; 63pp; English.

XX PCR primers AAC62131-33 were used to amplify the left and right ends
 CC of the bovine adenovirus type 1 (BAV-1) genome. BAV-1 exhibits a complex
 CC sequence organisation at its left and right ends. The genome exhibits an
 CC inverted terminal repeat (ITR) of 578 bp. A sequence of 419 bp is
 CC repeated twice at the left end of the genome. A single inverted copy of
 CC this repeat occurs at the right end of the genome. Foreign DNA sequence
 CC inserted into the early gene region 3 (E3) or E4 of BAV-1. The
 CC recombinant adenovirus is useful for inducing an immunological response
 CC in animals. The recombinant viruses are suitable as vaccines and for
 CC gene therapy.

XX Sequence 38 BP; 10 A; 7 C; 12 G; 9 T; 0 other;

Query Match 0.9%; Score 21.8; DB 21; Length 38;

Best Local Similarity 78.8%; Pred. No. 6e+04; 7; Indels 0; Gaps 0;

OY 1417 GCTTAGGCGAGATTTTCATGCAAAAGTCTCAT 1449
 |||| |||| |||| |||| ||||
 Db 37 GCGTAGCTCAGCTGTCTCATCCAAAGATCTCAT 5

RESULT 24
 AAT78318/C

ID AAT78318 standard; DNA; 46 BP.

AC AAT78318;

DT 13-OCT-1997 (first entry)

DE Plasmid vector pZgpt-a construction oligonucleotide oelp1.1.

KW Recombinant eukaryotic cytoplasmic DNA virus; vaccine production;

KW double selection marker; attenuated live pox virus; HIV; HBV;
 KW surface antigen gene; encephalitis; tick-borne; ss.

OS Synthetic.

XX EP753581-A1.

PD 15-JAN-1997.

PF 10-JUL-1995; 95EP-0110727.

PR 10-JUL-1995; 95EP-0110727.

XX (IMMO) IMMUNO AG.

PI Antoine G, Dörner F, Eibl J, Falkner F, Scheiflinger F;

DR WPI; 1997-079382/08.

PT Prodn. of recombinant eukaryotic cytoplasmic DNA viruses for vaccine
 PT prodn. - using novel construct contg. foreign DNA and double
 PT selection marker

XX Example 1; Page 8; 68pp; English.

XX A method has been produced for the production of recombinant eukaryotic
 CC cytoplasmic DNA viruses for vaccine production. The method involves
 CC inserting a construct DNA molecule into the genome of a eukaryotic
 CC cytoplasmic DNA virus, transfecting cells with the virus, and selecting
 CC a recombinant virus that does not contain the double selection marker
 CC cassette from the construct DNA. The DNA molecule preferably contains
 CC one or more foreign DNA segments of a gene encoding an antigen of a
 CC pathogen (especially HIV env, HIV gag, HIV gp120, HIV nef, HIV
 CC preS1-S2-S surface antigen gene, HBV S1-S2-S surface antigen gene, HBV
 CC S surface antigen gene, tick-borne encephalitis prem gene or tick-borne
 CC encephalitis E gene), and has a double selection marker cassette which
 CC is flanked by at least two direct repeat DNA sequences, where at least
 CC one foreign DNA segment does not occur within the DNA sequence bounded
 CC by the direct repeat sequences and where the double selection marker
 CC cassette comprises a dominant selection marker gene and a colour
 CC selection marker gene (preferably the colour selection marker is the
 CC Escherichia coli lacZ gene and the dominant selection marker is the
 CC E.coli hph or gpt gene). The present sequence represents the oelp1.1
 CC oligonucleotide used in the construction of the plasmid vector pZgpt-a.
 CC The DNA constructs and method are used for the production of vaccines,
 CC especially containing an attenuated live recombinant pox virus.

XX Sequence 46 BP; 21 A; 3 C; 5 G; 17 T; 0 other;

Query Match 0.9%; Score 21.8; DB 18; Length 46;

Best Local Similarity 70.7%; Pred. No. 6.6e+04; 12; Indels 0; Gaps 0;

OY 2063 TCGCAAAATCTGTTATACCTTTAAATATATCTGGAACCTTTT 2103
 |||| |||| |||| |||| ||||
 Db 46 TGTAACTATTTATATATGATGATGATATATATTTCAACTTTT 6

RESULT 25
 ABN71653/C

ID ABN71653 standard; DNA; 49 BP.

AC ABN71653;

DT 01-JUL-2002 (first entry)

DE Streptococcus agalactiae PCR primer SEQ ID NO 11093.

KW Streptococcus: GAS; GBS; group B streptococcus; Streptococcus agalactiae;

KW group A streptococcus; Streptococcus pyogenes; antibacterial; PCR; ss;

KW antiinflammatory; Infection; vaccine; meningitis; gene therapy; primer.

OS Streptococcus agalactiae.

OS Synthetic.
 XX WO200234771-A2.
 XX
 PD 02-MAY-2002.
 XX
 XX 29-OCT-2001; 2001WO-GB04789.
 PF
 XX 27-OCT-2000; 2000GB-0026333.
 PR 24-NOV-2000; 2000GB-0028727.
 PR 07-MAR-2001; 2001GB-0005640.
 XX
 PA (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 XX
 PI Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;
 PI Tetteijn H;
 XX WPI: 2002-352536/38.
 DR
 XX
 XX
 PT New Streptococcus protein for the treatment or prevention of infection
 PT or disease caused by Streptococcus bacteria, such as meningitis, and
 PT for detecting a compound that binds to the protein -
 PS
 XX Claim 8; Page 4492; 4525pp; English.
 XX
 XX The invention relates to a protein (ABP25413-ABP30895) from group B
 CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (SI), given in
 CC the specification. The proteins have antibacterial and antiinflammatory
 CC activity. (I), nucleic acids encoding (I), ABN6044-ABN71526 and
 CC antibodies that bind (I) are used in the manufacture of medicaments for
 CC the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a
 CC biological sample. (I) is used to determine whether a compound binds to
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
 CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic
 CC acid encoding (I) may be used to recombinantly produce (I) and may be
 CC used in gene therapy. Antibodies to (I) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 CC Streptococcus proteins. The present sequence is that of a PCR primer,
 CC useful to the invention.
 CC
 XX Sequence 49 BP; 23 A; 9 C; 10 G; 7 T; 0 other;
 SQ
 Query Match 0.9%; Score 21.8; DB 24; Length 49;
 Best Local Similarity 70.7%; Pred. No. 6.8e+04;
 Matches 29; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 OY 2100 TTTTGAATTATTCAGCCTTATTTGAGTAATAATTTCT 2140
 DB 45 TTTTGTGATTGTTCAGAGCCTGCTTTTGTACAACTTGT 5
 RESULT 26
 AAT78315
 ID AAT78315 standard; DNA; 49 BP.
 AC AAT78315;
 XX
 XX 13-OCT-1997 (first entry)
 DE Plasmid vector pZgt-a construction oligonucleotide elp1.21.
 XX
 XX Recombinant eukaryotic cytoplasmic DNA virus; vaccine production;
 KM double selection marker; attenuated live pox virus; HIV; HBV;
 KM surface antigen gene; encephalitis; tick-borne; ss.
 XX
 OS Synthetic.
 XX
 PN BP753581-A1.

XX
 PD 15-JAN-1997.
 XX
 PF 10-JUL-1995; 95EP-0110727.
 XX
 PR 10-JUL-1995; 95EP-0110727.
 XX
 PA (IMMO) IMMUNO AG.
 XX
 PI Antoine G, Dörner F, Eibl J, Falkner F, Schefflinger F;
 DR WPI: 1997-079382/08.
 XX
 XX
 PT Prodn. of recombinant eukaryotic cytoplasmic DNA viruses for vaccine
 PT Prodn. - using novel construct contg. foreign DNA and double
 PT selection marker
 XX
 XX Example 1; Page 8; 68pp; English.
 PS
 XX A method has been produced for the production of recombinant eukaryotic
 CC cytoplasmic DNA viruses for vaccine production. The method involves
 CC inserting a construct DNA molecule into the genome of a eukaryotic
 CC cytoplasmic DNA virus, transfecting cells with the virus, and selecting
 CC a recombinant virus that does not contain the double selection marker
 CC cassette from the construct DNA. The DNA molecule preferably contains
 CC one or more foreign DNA segments of a gene encoding an antigen of a
 CC pathogen (especially HIV env, HIV gag, HIV gp120, HIV nef, HBV
 CC S surface antigen gene, tick-borne encephalitis prem gene or tick-borne
 CC encephalitis E gene), and has a double selection marker cassette which
 CC is flanked by at least two direct repeat DNA sequences, where at least
 CC one foreign DNA segment does not occur within the DNA sequence bounded
 CC by the direct repeat sequences and where the double selection marker
 CC cassette comprises a dominant selection marker gene and a colour
 CC selection marker gene (preferably the colour selection marker is the
 CC Escherichia coli lacZ gene and the dominant selection marker is the
 CC E.coli hph or gpt gene). The present sequence represents the elp1.21
 CC oligonucleotide used in the construction of the plasmid vector pZgt-a.
 CC The DNA constructs and method are used for the production of vaccines,
 CC especially containing an attenuated live recombinant pox virus.
 XX
 XX Sequence 49 BP; 17 A; 8 C; 3 G; 21 T; 0 other;
 SQ
 Query Match 0.9%; Score 21.6; DB 18; Length 49;
 Best Local Similarity 68.2%; Pred. No. 7.7e+04;
 Matches 30; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
 OY 2060 ATGTGCAAAATCTGTATACCTTAAATATATATGCACTTT 2103
 DB 2 ATTCGTTAACTTATTTATAGCATAGAAATATATTTCAACTTT 45
 RESULT 27
 AAF69254/C
 ID AAF69254 standard; DNA; 45 BP.
 AC AAF69254;
 XX
 XX 17-APR-2001 (first entry)
 DE Primer used in affinity-improved anti-IgE antibody generation SEQ ID 27.
 XX
 XX Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological;
 KM antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;
 KM conjunctivitis; eczema; urticaria; food allergy; ss.
 XX
 OS Synthetic.
 XX
 PN US6172213-B1.
 XX
 PD 09-JAN-2001.
 XX
 PF 30-JUN-1998; 98US-0109207.

```
XX 02-JUL-1997; 97US-0051554.
PR (GETH ) GENENTECH INC.
XX
XX Lowman HB, Presta LG, Jardieu PM, Lowe J;
PI WPI: 2001-122353/13.
XX
XX New nucleic acid encoding anti-immunoglobulin E antibody with improved
PT properties, produced by substituting aspartyl residues in unimproved
PT immunoglobulin E prone to isomerization by other residues by affinity
PT maturation with phage display
PS
XX Example 4: Column 73-74; 87pp; English.
XX
XX This invention relates to a nucleotide sequence encoding an antibody
CC with improved anti-1gE antibody activity. The antibody has improved
CC action due to a process comprising, a) identifying aspartyl residues
CC prone to isomerization in unimproved anti-1gE (immunoglobulin E)
CC antibody; b) substituting alternative residues to create candidate
CC molecules; and c) selecting those candidate molecules which display
CC affinity against the target molecule. Use of the antibody results in
CC antiasthmatic; antiallergic; ophthalmological; dermatological and
CC antiinflammatory activity. The antibodies are useful for treating
CC IgE-mediated disorders such as asthma, allergic rhinitis, conjunctivitis,
CC eczema, urticaria and food allergies. The mutant antibodies produced by
CC the above mentioned nucleic acids may also be used as affinity
CC purification agents and in diagnostic assays for detecting the expression
CC of an antigen of interest in specific cell, tissues or serum. Amino acid
CC sequences AAB76936-AAB76960 represent fragments of anti-1gE antibodies of
CC the invention. Polynucleotide sequence AAF69253 represents an expression
CC plasmid used in the course of the invention, and oligonucleotides
CC - AAF69254 - AAF69271 are used in the generation of affinity improved
CC anti-1gE antibodies.
XX
XX Sequence 45 BP; 15 A; 9 C; 10 G; 11 T; 0 other;
SQ
XX
XX Query Match 0.9%; Score 21.4; DB 22; Length 45;
Best Local Similarity 71.8%; Pred. No. 8.3e+04;
Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
OY 1201 CTGTTACCTTGTTAATAGACTTAATACATGCAACAGAG 1239
DB 41 CTATCACCCTTCTATTAGACTTATTAAGTCGACGACGACAG 3
XX
XX RESULT 28
AAF77140
ID AAF77140 standard; DNA; 48 BP.
XX
XX AAF77140;
XX
XX 22-MAY-2001 (first entry)
XX
XX R-structure nucleotide #9.
XX
XX Resonating; R-structure; tertiary structure; anti-viral; ss.
XX
XX Ebola virus.
XX
XX US6194155-B1.
XX
XX 27-FEB-2001.
XX
XX 05-MAY-1999; 99US-0305408.
XX
XX 05-MAY-1999; 99US-0305408.
XX
XX (COHE/) COHEN J.
XX
XX Cohen J;
XX
```

```
DR WPI: 2001-234428/24.
XX
XX Computerized method for identifying and locating resonating,
PT self-hybridizing nucleic acid elements comprises employing a
PT device, which has computer program instructions for creating data
PT structures and operator modules
XX
XX Example 1; Column 11-12; 21pp; English.
XX
XX The present invention relates to identifying resonating,
CC self-hybridizing molecular genetic nucleotide structures
CC (R-structures) in a nucleic acid sequence, employing a
CC memory device. The method is also useful for identifying
CC viral nucleic acid sequences that form tertiary structures.
CC The ability to identify such structures or sequences may
CC lead to faster development of anti-viral therapies.
XX
XX Sequence 48 BP; 20 A; 7 C; 5 G; 16 T; 0 other;
SQ
XX
XX Query Match 0.9%; Score 21.4; DB 22; Length 48;
Best Local Similarity 71.8%; Pred. No. 8.6e+04;
Matches 28; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
OY 1023 CTTTGAATATTTCAGAAATTCCTCCAGATTTTAATTTC 1061
DB 2 CTTTAAATATTTAAGAAACTGACGACATTAATTC 40
XX
XX RESULT 29
AAL28758
ID AAL28758 standard; DNA; 50 BP.
XX
XX AAL28758;
XX
XX 24-JAN-2002 (first entry)
XX
XX Human SNP oligonucleotide #1966.
XX
XX
XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
XX neutroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
XX amyloid protein; angiotensin; apoptosis related protein; cadherin;
XX cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
XX complement related protein; cytochrome; kinase; cytokine; interferon;
XX interleukin; G-protein coupled receptor; thioesterase; inflammation;
XX multifactorial disease; autoimmune disease; infection;
XX nervous system disease; ss.
XX
XX Homo sapiens.
XX
XX WO200147944-A2.
XX
XX 05-JUL-2001.
XX
XX 28-DEC-2000; 2000WO-US35498.
XX
XX 28-DEC-1999; 99US-0173419.
XX
XX 27-DEC-2000; 2000US-0173419.
XX
XX (CDRA-) CDRAGEN CORP.
XX
XX Shimkets RA, Leach M;
XX
XX WPI: 2001-465210/50.
XX
XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g.
PT cancer, autoimmune diseases and infections
XX
XX Claim 1; Page 1944; 4143pp; English.
XX
XX The present invention relates to oligonucleotides encoding polymorphic
CC variants of proteins related to amylases, amyloid proteins, angiotensin,
CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
```

CC histones, kinases, colony stimulating factors, complement related
 CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
 CC G-protein coupled receptors and thioesterases. The present sequence is
 CC one such oligonucleotide. The oligonucleotides and the peptides encoded
 CC by them may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate expression of the proteins listed
 CC above. Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
 CC leukemia), diseases of the nervous system and an infection of pathogenic
 CC organisms.

XX Sequence 50 BP; 21 A; 8 C; 6 G; 15 T; 0 other;

Query Match 0.9%; Score 21.4; DB 22; Length 50;

Best Local Similarity 66.0%; Pred. No. 8.7e+04; Mismatches 16; Indels 0; Gaps 0;

Matches 31; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

1472 TAATGATTCTGATATGATCCATCAGATCCAGTCTGGAACACAGAA 1518

1 TATACATTCAGATATGTTGAAACATTTTAAGCTACAAACAGAA 47

RESULT 30

AAH29638

ID AAH29638 standard; DNA; 47 BP.

XX AAH29638;

XX 17-JUL-2001 (first entry)

XX Drosophila melanogaster essential gene fragment, SEQ ID NO: 827.

XX Drosophila melanogaster; fruit fly; essential gene; screening assay;

KW pesticide; crop protection; chromosome 2; ds.

XX Drosophila melanogaster.

XX PN - WO200118547-A1.

XX 15-MAR-2001.

XX 06-SEP-2000; 2000WO-GB03444.

XX 07-SEP-1999; 99GB-0021009.

XX (UNIT) UNIV GLASGOW.

XX Davies RW, Kaiser K, Yang MY;

XX WPI: 2001-281436/29.

XX Screening assays for used for identifying compounds having a
 PT physiological effect on proteins identified as being essential -

XX Claim 1; Page 642; 695pp; English.

XX The present sequence is part of an essential gene from Drosophila
 CC melanogaster. Lack of expression of the protein encoded by this
 CC gene leads to a lethal or semi-lethal phenotype. The invention
 CC relates to 902 nucleic acid sequences from genes encoding proteins
 CC which are thought to be essential, and to a screening assay for
 CC identifying compounds which have a physiological effect on these
 CC proteins. Suitable compounds are useful as pesticides and may be used
 CC in conjunction with other pesticides and herbicides for crop
 CC protection. The gene corresponding to the present sequence is located
 CC on chromosome 2.

XX Sequence 47 BP; 13 A; 6 C; 9 G; 19 T; 0 other;

Query Match 0.9%; Score 21.2; DB 22; Length 47;

Best Local Similarity 69.0%; Pred. No. 9.5e+04; Mismatches 29; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

OY 2041 AACATCTGTTTGGCTTTATGTCACAAATCTGTATAGCTT 2082

5 AGCCATATTAAGTGTGTATTTGCAAAAGTTGTATATGATT 46

RESULT 31

AAH6939/C

ID AAH6939 standard; DNA; 48 BP.

XX AAH6939;

XX 15-JAN-2001 (first entry)

XX TPOX allele oligonucleotide.

XX Detection; nucleic acid hybrid; depolymerisation; analysis; SNP;

KW single nucleotide polymorphism; identification; viral load; probe;

KW genotyping; medical marker diagnostic; primer; target; mutation;

XX genetic disease; ss.

XX Synthetic.

XX WO200049180-A1.

XX 24-AUG-2000.

XX 18-FEB-2000; 2000WO-US04242.

XX 18-FEB-1999; 99US-0252436.

XX 21-JUL-1999; 99US-0358972.

XX 25-AUG-1999; 99US-0383316.

XX (PROM) - PROMEGA CORP.

XX Shultz JW, Lewis MK, Leippe D, Mandrekar M, Kephart D, Rhodes RB;

PI Andrews CA, Hartnett JR, Gu T, Olson RJ, Wood KV, Welch R;

XX WPI: 2000-565377/52.

XX Determining presence or absence of a predetermined endogenous nucleic

XX acid sequence by using an enzyme that depolymerizes the 3' end of an

XX oligonucleotide probe hybridized to a target sequence to release

XX identifier nucleotides

XX Example: Page 338; 389pp; English.

XX The present invention describes a method (M1) for determining the
 CC presence or absence of a predetermined endogenous nucleic acid target
 CC sequence (ENAT). The method comprises hybridizing a probe having an
 CC identifier nucleotide (IN) with ENAT which is treated with an enzyme
 CC that depolymerizes the 3' end of hybridised NA to release the INs.
 CC M1 is used for determining the number of known sequence repeats present
 CC in a nucleic acid target sequence in a nucleic acid sample. The method
 CC is also useful for determining whether a nucleic acid target sequence in
 CC a sample is an allele from a homozygous or heterozygous locus. The
 CC method is also useful for detection of mutations, translocations and
 CC SNPs in nucleic acids (including those associated with genetic disease),
 CC determination of viral load, species identification, sample
 CC contamination, and analysis of forensic samples. AAH6791 to AAH7079
 CC and AAH12817 represent sequence which are used in the exemplification of
 CC the present invention.
 CC N.B. There is a discrepancy between the SEQ ID NO: and sequences given
 CC in the examples, and the SEQ ID NO: and sequences given in the sequence
 CC listing from the present invention.

XX Sequence 48 BP; 18 A; 7 C; 11 G; 12 T; 0 other;

Query Match 0.9%; Score 21.2; DB 21; Length 48;

Best Local Similarity 69.0%; Pred. No. 9.6e+04; Mismatches 29; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

PR 10-JUL-1995; 95EP-0110727.
XX
XX (IMMO) IMMUNO AG.
XX
XX Antoine G, Dörner F, Eibl J, Falkner F, Scheiflinger F;
XX WPI, 1997-079382/08.
DR
XX
XX Prod. of recombinant eukaryotic cytoplasmic DNA viruses for vaccine
PT Prod. - using novel construct contg. foreign DNA and double
PT selection marker
XX
XX Example 1; Page 8; 68pp; English.
PS
XX
XX A method has been produced for the production of recombinant eukaryotic
CC cytoplasmic DNA viruses for vaccine production. The method involves
CC inserting a construct DNA molecule into the genome of a eukaryotic
CC cytoplasmic DNA virus, transfecting cells with the virus, and selecting
CC a recombinant virus that does not contain the double selection marker
CC cassette from the construct DNA. The DNA molecule preferably contains
CC one or more foreign DNA segments of a gene encoding an antigen of a
CC pathogen (especially HIV env, HIV gag, HIV gagpol, HIV tat, HIV
CC pps1-52-S surface antigen gene, HBV S1-S2-S surface antigen gene, HBV
CC S surface antigen gene, tick-borne encephalitis prem gene or tick-borne
CC encephalitis E gene), and has a double selection marker cassette which
CC is flanked by at least two direct repeat DNA sequences, where at least
CC one foreign DNA segment does not occur within the DNA sequence bounded
CC by the direct repeat sequences and where the double selection marker
CC cassette comprises a dominant selection marker gene and a colour
CC selection marker gene (preferably the colour selection marker is the
CC Escherichia coli lacZ gene and the dominant selection marker is the
CC E. coli hph or gpt gene). The present sequence represents the elp1.11
CC oligonucleotide used in the construction of the plasmid vector ppgpt-a.
CC The DNA constructs and method are used for the production of vaccines,
CC especially containing an attenuated live recombinant pox virus.
XX
SQ Sequence 45 BP; 19 A; 3 C; 8 G; 15 T; 0 other;
Query Match 0.9%; Score 21; DB 18; Length 45;
Best Local Similarity 73.0%; Pred. No. 1.1e+05;
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 2067 AAATCTGTTAGCTTAAATATATATCTGGAACCTTT 2103
DB 41 AACCTATTATAGCATGAATATATATTTTCACTTTT 5
RESULT 35
AAAS6041/C
ID AAAS6041 standard; DNA; 47 BP.
XX
XX AAAS6041;
XX
XX 05-SEP-2000 (first entry)
XX
XX Plasmid pKK223-3-lacZ construction PCR primer SEQ ID NO:13.
XX
XX Escherichia coli; E. coli; randomised peptide library; identification;
XX stabilised bioactive peptide; synthesis; intracellular selection;
XX screening; lac operon; protease resistant; peptidease resistant;
XX Rop protein; glutathione sulphotransferase; thiorodoxin; infection;
XX maltose binding protein; glutathione reductase; antimicrobial;
XX antibacterial; PCR primer; ss.
XX
XX Escherichia coli.
XX Synthetic.
XX
XX WO200022112-A1.
XX
XX 20-APR-2000.
XX
XX 12-OCT-1999; 99WO-US23731.
XX
XX

PR 13-OCT-1998; 98US-0104013.
XX
XX 14-DEC-1998; 98US-0112150.
XX
XX (UIGE-) UNIV GEORGIA RES FOUND INC.
XX (ALTM/ ALTMAN E.
XX
XX Altman E;
XX
XX WPI, 2000-317972/27.
DR
XX
XX Identifying recombinantly an antimicrobial bioactive peptide used as a
PT therapeutic agent involves transforming a host cell with expression
PT vector with tightly regulable control region and measuring its
PT inhibition
XX
XX Example 1; Page 36; 135pp; English.
PS
XX
XX The present invention describes a method for identifying a bioactive
CC peptide (BP) involving transforming a cell with an expression vector
CC comprising a tightly regulable control region operably linked to a
CC nucleic acid sequence encoding a peptide (P), growing the transformed
CC cell under conditions that repress expression of (P) and then inducing
CC its expression which, if is inhibitory to host cell growth is
CC indicative of BP expression. An antimicrobial peptide from the present
CC invention, which is stabilised, is used for treating a patient having a
CC condition treatable with a peptide drug. The stabilised peptides are
CC also used for inhibiting the growth of a microbe. The new antibacterial
CC peptides are useful to treat various pathogenic bacteria such as
CC Staphylococci, Streptococci and Enterococci which are the primary causes
CC of nosocomial infections. Novel inhibitor peptides identified by the
CC method can be medical treatments and therapies directed against
CC microbial infection. Also, these novel inhibitor peptides can be used,
CC in turn, to identify additional novel antibacterial peptides using a
CC synthetic approach, and can also be used to elucidate potential new drug
CC targets. The inhibitor peptide target which is inactivated is identified
CC using reverse genetics by isolating mutants that are no longer inhibited
CC by the peptide. These mutants are then mapped in order to precisely
CC determine the protein target that is inhibited. AAAS6033 to AAAS6106 and
CC AAAY90964 to AAAY90999 are sequences used in the exemplification of the
CC present invention.
XX
SQ Sequence 47 BP; 15 A; 10 C; 10 G; 12 T; 0 other;
Query Match 0.9%; Score 21; DB 21; Length 47;
Best Local Similarity 66.7%; Pred. No. 1.1e+05;
Matches 30; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 1238 AGTGACTTCTGGAGAAAGCTGATGCTGTCTCAGTCGAAATGGT 1282
DB 46 AGTGAATCCGTAATCATGTGATGCTGTCTCAGATCAT 2
RESULT 36
AAI75434/C
ID AAI75434 standard; DNA; 50 BP.
XX
XX AAI75434;
XX
XX 09-NOV-2001 (first entry)
XX
XX Human silent SNP containing nucleic acid SEQ.2375.
XX
XX Human; single nucleotide polymorphism; SNP; genome; gene therapy;
XX protein therapy; vaccine; probe; diagnostic assay; detection;
XX quantitation; restorative therapy; polymorphic; ds.
XX
XX Homo sapiens.
XX
XX WO200140521-A2.
XX
XX 07-JUN-2001.
XX
XX 30-NOV-2000; 2000WO-US32758.
XX
XX

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XX 30-NOV-1999; 99US-0168138.
PR 29-NOV-2000; 2000US-0726173.
XX (CURA-) CUNAGEN CORP.
XX Shinkets RA, Leach M;
XX WPI, 2001-356160/37.
XX Polymorphic nucleic acid sequences, useful in genetic testing and
PT therapy -
XX Claim 1; Page 778; 2653pp; English.
XX AA173060 to AA179867 represent isolated human polymorphic polynucleotide
CC sequences (I), which contain single nucleotide polymorphisms (SNPs).
CC AA53114 to AA53329 represent peptides related to human polymorphic
CC polynucleotide sequences. The sequences can be used in gene and protein
CC therapy, and in vaccine production. (I) and the polypeptides encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate expression of polymorphic polypeptides.
CC For example, (I) may be used to treat disorders by rectifying mutations
CC or deletions in a patient's genome that affect the activity of
CC polypeptides by expressing inactive proteins or to supplement the
CC patients own production of polypeptide. Additionally, (I) and its
CC complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar nucleic acids
CC in samples, and therefore which patients may be in need of restorative
CC therapy. The polypeptides encoded by (I) may be used as antigens in the
CC production of antibodies specific for polymorphic polypeptides. The
CC antibodies may also be used to down regulate expression and activity.
CC The antibodies may also be used as diagnostic agents for detecting the
CC presence of polymorphic polypeptides in samples.
XX
XX Sequence 50 BP; 20 A; 12 C; 7 G; 11 T; 0 other;
SQ
Query Match 0.9%; Score 21; DB 22; Length 50;
Best Local Similarity 73.0%; Pred. No. 1.1e+05;
Matches 27; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 2171 TATGCAAGATTTTGGCAGCTTTGTTTCAAGATG 2207
| ||||| ||| ||| ||| ||| ||| |||
Db 38 TGTGCAAGATTTTGTGTGTTTAAAGCTG 2

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XX WPI; 2000-376481/32.
XX Human prostate cancer (HPC2) nucleic acids, polypeptides, and
PT antibodies, useful for treatment and diagnosis of prostate cancer -
XX
XX Example 5; Page 60; 157pp; English.
XX
XX The present sequence is a primer used in the isolation of the human
CC and murine prostate cancer predisposing genes HPC2 and Mm.HPC2. The human
CC version of the gene is found on chromosome 17p. Some alleles cause a
CC predisposition to cancer, particularly prostate cancer. This gene and its
CC protein can be used in peptide and gene therapy for cancer patients, as
CC well as being useful as diagnostic tools (both for cancer sufferers and
CC those with a predisposition to the disease) and in the production of
CC cancer drugs.
XX
XX Sequence 41 BP; 13 A; 8 C; 10 G; 10 T; 0 other;
SQ
Query Match 0.9%; Score 20.8; DB 21; Length 41;
Best Local Similarity 70.0%; Pred. No. 1.1e+05;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 1231 CAACAGAGTACTCTGTGAGAAAGCTCATGGCTGTC 1270
| ||||| ||| ||| ||| ||| ||| |||
Db 41 CTACAGACACCACTTTGAAGCATGCTCATGCTGTTCC 2

```

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RESULT 37
AA560309/C
ID AAA60309 standard; DNA: 41 BP.
XX
XX AAA60309;
XX
XX 07-DEC-2000 (first entry)
XX
XX Human HPC2 CDNA exon 10 mutation screening primer SEQ ID NO: 130.
DE
XX Human: mouse; prostate cancer predisposing gene; HPC2;
KW human chromosome 17p; gene therapy; peptide therapy; drug design;
KW PCR primer; sequencing primer; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200027864-A1.
PN
XX 18-MAY-2000.
PD
XX
XX 05-NOV-1999; 99WO-US26055.
PF
XX
XX 06-NOV-1998; 98US-0107468.
PR
XX (MYRI-) MYRIAD GENETICS INC.
PA
XX
XX Tavligian SV, Teng DHF, Simard J, Rommens JM;

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RESULT 38
AAS99044/C
ID AAS99044 standard; DNA: 41 BP.
XX
XX AAS99044;
XX
XX 12-MAR-2002 (first entry)
XX
XX Human prostate cancer predisposing gene (HPC2) PCR primer #40.
DE
XX
XX Human: mouse; HPC2; prostate cancer; neoplastic growth; cytostatic; ss;
KW gene therapy; prostate cancer predisposing gene; chimpanzee; gorilla;
KW sequencing primer; PCR primer.
XX
XX Homo sapiens.
OS
XX
XX WO200185911-A2.
PN
XX
XX 15-NOV-2001.
PD
XX
XX 07-MAY-2001; 2001WO-US14602.
PF
XX
XX 05-MAY-2000; 2000US-0564805.
PR
XX
XX (MYRI-) MYRIAD GENETICS INC.
PA (HOSP-) HOSPITAL FOR SICK CHILDREN.
XX
XX Tavligian SV, Teng DHF, Simard J, Rommens JM;
XX
XX WPI; 2002-066599/09.
XX
XX Novel nucleic acid sequence encoding HPC2 polypeptide, which is marker
PT for prostate cancer, is useful in gene therapy techniques to restore
PT HPC2 normal levels by which neoplastic growth is suppressed in
PT recipient cell -
XX
XX Example 8; Page 73; 239pp; English.
XX
XX The invention relates to a human prostate cancer predisposing gene coding
CC for an HPC2 polypeptide. The DNA and protein sequences are useful as
CC diagnostic reagents for identifying a mutant HPC2 nucleotide sequence in
CC a suspected mutant HPC2 allele by comparing the sequence of the suspected
CC mutant HPC2 allele with a wild-type HPC2 sequence. The sequences are also
CC useful for detecting an alteration in HPC2, where the alteration is
CC associated with cancer in a human. The method involves analysing an HPC2

```


CC gene or an HPC2 gene expression product from a tissue of the human. The
 CC HPC2 gene is useful as a marker for prostate cancer and can be used in
 CC gene therapy techniques to suppress neoplastic growth of recipient cells
 CC which carry the mutant HPC2 allele. The sequences represent primers used
 CC in the methods of the invention, cDNA encoding human and mouse HPC2 and
 CC cDNA encoding HPC2 paralogues and orthologues.

XX Sequence 41 BP; 13 A; 8 C; 10 G; 10 T; 0 other;

Query Match 0.9%; Score 20.8; DB 24; Length 41;
 Best Local Similarity 70.0%; Pred. No. 1.1e+05;
 Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1231 CAACAGAGTGTCTGGAGAAAGCTCATGCTGTCC 1270
 DB 41 CTACAGACACCACTTTGAAGAGTGTATGCTTTCC 2

RESULT 39

AAF29312 standard; DNA; 48 BP.

XX AAF29312;

XX 18-APR-2001 (first entry)

DE Primer base sequence used to illustrate primer selection method.

XX Primer; optimum sequence; differential display; ss.

XX Synthetic.

PN JP2000308487-A.

PD 07-NOV-2000.

PF 30-MAR-1999; 99JP-0088410.

PR 30-MAR-1999; 99JP-0088410.

XX (KAGA-) KAGAKU GIUTTSU SHINKO JIGYODAN.

XX WPI; 2001-046077/06.

PT Selection of primer base for optimizing primer selection comprises

PT obtaining an optimum sequence for differential display from an

PT expression gene data base -

XX Disclosure; Fig 9; 13pp; Japanese.

CC This invention relates to a method for selecting the sequence of a

CC primer. The method comprises obtaining an optimum sequence for a

CC differential display from an expression gene data base, and using the

CC base sequences most frequently expressed as the primer candidates in the

CC order of frequency. The optimum primer group characterised by the use of

CC genetic algorithm from the primer candidates is selected. The method is

CC used for selecting a primer sequence quickly. The present sequence

CC represents a primer used in an illustration of the method of the

CC invention.

XX Sequence 48 BP; 18 A; 2 C; 5 G; 23 T; 0 other;

Query Match 0.9%; Score 20.8; DB 22; Length 48;
 Best Local Similarity 70.0%; Pred. No. 1.2e+05;
 Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1000 TTAATGATCACAATTTTATGCTTGAATATTCAGA 1039
 DB 3 TTAATGAGAAATTTTATTTTAAATGAAGATTCAAA 42

RESULT 40
 ABN71922/c

ID ABN71922 standard; DNA; 48 BP.

XX ABN71922;

XX 01-JUL-2002 (first entry)

DE Streptococcus agalactiae PCR primer SEQ ID NO 11362.

XX Streptococcus; GAS; group B streptococcus; Streptococcus agalactiae;

XX group A streptococcus; Streptococcus pyogenes; antibacterial; PCR; ss;

XX antiinflammatory; infection; vaccine; meningitis; gene therapy; primer.

OS Streptococcus agalactiae.

OS Synthetic.

PN WO200234771-A2.

XX 02-MAY-2002.

XX 29-OCT-2001; 2001WO-GH04789.

XX 27-OCT-2000; 2000GB-0026333.

XX 24-NOV-2000; 2000GB-0028727.

XX 07-MAR-2001; 2001GB-0005640.

XX (CHIR-) CHIRON SPA.

XX (GENO-) INST GENOMIC RES.

XX Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;

XX Tetelin H;

XX WPI; 2002-352536/38.

XX New Streptococcus protein for the treatment or prevention of infection

PT or disease caused by Streptococcus bacteria, such as meningitis, and

PT for detecting a compound that binds to the protein -

XX Claim 8; Page 4499; 4525pp; English.

XX The invention relates to a protein (ABP25413-ABP30895) from group B

CC Streptococcus/GAS (Streptococcus agalactiae) or group A streptococcus/GAS

CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in

CC the specification. The proteins have antibacterial and antiinflammatory

CC activity. (1), nucleic acids encoding (1), ABR66044-ABN71526 and

CC antibodies that bind (1) are used in the manufacture of medicaments for

CC the treatment or prevention of infection or disease caused by

CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.

CC Nucleic acids encoding (1) are used to detect Streptococcus in a

CC biological sample. (1) is used to determine whether a compound binds to

CC (1). A composition comprising (1) or a nucleic acid encoding (1), may be

CC used as a vaccine or diagnostic composition. The disease caused by

CC Streptococcus that is prevented or treated may be meningitis. Nucleic

CC acid encoding (1) may be used to recombinantly produce (1) and may be

CC used in gene therapy. Antibodies to (1) are used for affinity

CC chromatography, immunoassays, and distinguishing/identifying

CC Streptococcus proteins. The present sequence is that of a PCR primer,

CC useful to the invention.

XX Sequence 48 BP; 17 A; 5 C; 11 G; 15 T; 0 other;

Query Match 0.9%; Score 20.8; DB 24; Length 48;
 Best Local Similarity 70.0%; Pred. No. 1.2e+05;
 Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 2101 TTTAGATTATCCAGCCTTATTTGAGTAATATTGT 2140
 DB 44 TATATAAATGTTCACAGCCTGCTTTTGTACAAACTGT 5

RESULT 41
 AAT04944/c
 ID AAT04944 standard; DNA; 49 BP.
 XX

AC	AAT04944;
XX	
DT	05-JUN-1996 (first entry)
XX	
DE	Synthetic promoter operable in B. subtilis and E. coli.
XX	
KW	Plasmid vector; pSM671; promoter; B. subtilis; E. coli;
KW	hydantoinase; carboxylase; alpha-amylase; beta-amylase;
KM	isoamylase; interleukin; interferon; hormones; recombinant;
KW	antibodies; ss.
XX	
OS	Synthetic.
FH	
FT	Key Location/Qualifiers
FT	-35_signal 15..20
FT	/tag= a
FT	-10_signal 39..44
FT	/tag= b
PN	EP681027-A2.
PD	08-NOV-1995.
PF	01-MAR-1995; 95EP-0102876.
PR	15-APR-1994; 94IT-OMI0727.
PA	(ENIE) ENRICERCHE SPA.
PI	Fraschetti G, Grandi G;
DR	WPL: 1995-375209/49.
PS	New plasmid vector contg. synthetic promoter for E.coli and B.subtilis - capable or directing high expression of an heterologous gene under control of the promoter
Example 1; Page 9; 14pp; English.	
The plasmid vector pSM671 for the expression of heterologous proteins, contains AAT04944 which comprises a promoter operable in B. subtilis and E. coli (AAT04944), the bond site of the mRNA to be expressed at the ribosome and the multiple cloning site of the plasmid pUC18. pSM671 is stable in E. coli and B. subtilis, and the promoter can direct high level expression of heterologous proteins (over 5% total proteins). The heterologous proteins include hydantoinase, carboxylase, alpha/beta-amylase, isoamylase, interleukin, interferon, hormones or recombinant antibodies.	
Sequence 49 BP; 18 A; 3 C; 6 G; 22 T; 0 other;	
Query Match 0.9%; Score 20.8; DB 16; Length 49; Best Local Similarity 64.6%; Pred.No.1.2e+05;	
Matches 31; Conservative 0; Mismatches 17; Indels 0; Gaps 0;	
QY 2068 AATCGTATAAGCTTAATAATATATCAGCACTTTTGATTATTCACA 2115 Dd 49 AATCATATTATGACTAAAAAATTTCCTGAACCAATATTAATTTTCTCA 2	
RESULT 42	
ID AAL29418/c	
XX AAL29418 standard; DNA; 50 BP.	
XX	
DT 24-JAN-2002 (first entry)	
DE Human SNP oligonucleotide #2626.	
Immunosuppressive; immunostimulatory; anti-inflammatory; cytotoxic; neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiotensin; apoptosis related protein; cadherin;	

KM	cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinesin; cytokine; interferon; interleukin; G-protein coupled receptor; thioesterase; inflammation; multifactorial disease; autoimmune disease; infection;
KM	nervous system disease; ss.
OS	
XX	Homo sapiens.
XX	
PN	MO200147944-A2.
XX	
PD	05-JUL-2001.
XX	
XX	28-DEC-2000; 2000WO-US54598.
XX	
PR	28-DEC-1999; 99US-0173419.
PR	27-DEC-2000; 2000US-0173419.
XX	
PA	(CURA-) CURAGEN CORP.
XX	
PI	Shimkets RA, Leach M;
XX	
DR	WPI; 2001-465210/50.
PT	Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. cancer, autoimmune diseases and infections -
PT	
XX	
PS	Claim 1; Page 2137; 4143pp; English.
XX	
CC	The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amylases, amyloid proteins, angiopoietin, apoptosis related proteins, cachectin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-protein coupled receptors and thioesterases. The present sequence is one such oligonucleotide. The oligonucleotides and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the bladder, brain, breast, colon and kidney, organisms.
CC	
CC	
XX	
SO	Sequence 50 BP; 15 A; 4 C; 10 G; 21 T; 0 other;
	Query Match 0.98; Score 20.8; DB 22; Length 50;
	Best Local Similarity 64.68; Pred. No. 1.2e+05;
	Matches 31; Conservative 0; Mismatches 17; Indels 0; Gaps 0
QY	222 ACAACATGATTTGGAAAGCTGGCAATGCATCATATAAACAACA 269
Db	50 ACAACATGATTTCTTGAATAATATACCAAAATATCTTATCTATGAACTACA 3
RESULT 43	
ABL00257/c	
ID	ABL00257 standard; DNA; 50 BP.
AC	
XX	ABL00257;
XX	
DT	
XX	
DE	05-MAR-2002 (first entry)
XX	
XX	Human silent noncoding SNP oligonucleotide SEQ ID NO:248.
XX	
XX	Human; single nucleotide polymorphism; SNP; polymorphism; cytosolic; immunosuppressive; anti-inflammatory; neuroprotective; antimicrobial; autoimmune disease; inflammation; cancer; nervous system disease; infection; polymorphic protein; ds.
XX	
XX	Homo sapiens.

XX MO200138586-A2.
 XX 31-MAY-2001.
 XX 22-NOV-2000; 2000MO-US32311.
 XX 24-NOV-1999; 99US-0167383.
 XX (CURA-) CURAGEN CORP.
 XX Shinkets RA, Leach M;
 XX WPI; 2001-355949/37.
 XX Isolated human nucleic acids comprising one or more single nucleotide
 XX polymorphisms, useful for treating a subject suffering from a
 XX pathology, e.g. autoimmune diseases, ascribed to the presence of a
 XX sequence polymorphism -
 XX Claim 1; Page 322; 674pp; English.
 XX ABL00010 to ABL01104 represent human nucleic acid oligonucleotides
 XX comprising one or more single nucleotide polymorphisms (SNPs). ABB56531
 XX to ABB56903 represent human peptides encoded by some of the SNP
 XX oligonucleotides. The sequences from the present invention can have
 XX immunosuppressive, cytostatic, antiinflammatory, neuroprotective and
 XX antitubercular activities. Nucleic acids, polypeptides, oligonucleotides
 XX and antibodies from the present invention can be used for treating a
 XX subject suffering from, at risk for, or suspected of, suffering from a
 XX pathology ascribed to the presence of a sequence polymorphism. The
 XX pathology may be autoimmune diseases, inflammation, cancer, diseases of
 XX the nervous system, and infection by pathogenic microorganisms. The SNPs
 XX are also useful for determining which forms of a characterised
 XX polymorphism are present in individuals. The antibodies may be used in
 XX the detection, quantitation and/or cellular or tissue localisation of a
 XX polymorphic protein (e.g., for use in measuring levels of the
 XX polymorphic protein within appropriate physiological samples).
 XX Sequence 50 BP; 26 A; 5 C; 7 G; 12 T; 0 other;
 XX
 XX Query Match 0.9%; Score 20.8; DB 23; Length 50;
 XX Best Local Similarity 70.0%; Pred. No. 1.2e+05;
 XX Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 XX
 XX QY 2220 AATCTTGATAAATGACTGTTTCTGCTAATACTAA 2259
 XX 43 AATCTTTGATAAATGCTTTTCTGCTGAGATTTA 4
 XX
 XX RESULT 44
 XX ABR6581
 XX ID ABR6581 standard; DNA; 35 BP.
 XX ABR6581;
 XX 24-SEP-2002 (first entry)
 XX Newcastle disease virus nucleoprotein mutagenic PCR primer P3A.
 XX Nucleoprotein; NP; immunodominant epitope; newcastle disease; poultry;
 XX virucide; ND; vaccine; ovo administration; ss; PCR; primer.
 XX Newcastle disease virus.
 XX WO200236617-A2.
 XX 10-MAY-2002.
 XX 30-OCT-2001; 2001MO-EP12573.
 XX 02-NOV-2000; 2000EP-0203814.
 XX

PA (ALKU) AKZO NOBEL NV.
 XX Medabstion T, Koelen MM;
 XX WPI; 2002-527441/56.
 XX New Newcastle disease virus (NDV) mutant, useful as a vaccine for
 XX protecting poultry (e.g. chicken) against Newcastle disease or as a
 XX marker vaccine to distinguish vaccinated animals from those infected
 XX with naturally occurring NDV -
 XX Example 1; Page 15; 51pp; English.
 XX The invention relates to a Newcastle disease virus (NDV) mutant, which
 XX lacks an immunogenic epitope on a NDV protein as a result of a mutation
 XX in a gene encoding the protein, where the NDV mutant lacks an epitope
 XX located within a regions (amino acids 447-455 and 443-460) of the
 XX nucleoprotein (NP). Also included are a vaccine against Newcastle disease
 XX (ND) in poultry comprising the DNA mutant in a live or inactivated form,
 XX and a pharmaceutical carrier or diluent and determining NDV infection in
 XX poultry by examining a sample of the animal for the presence or absence
 XX of antibodies reactive with the immunodominant epitope located within the
 XX region of the NP. The NDV mutant is useful as a vaccine for protecting a
 XX poultry against ND. The NDV NP mutant is also useful for manufacturing a
 XX vaccine against ND in poultry, particularly for in ovo administration.
 XX The vaccine is also useful in a ND control program to distinguish
 XX vaccinated animals from animals infected with naturally occurring NDV.
 XX The NDV mutant is also useful as a marker vaccine to allow serological
 XX distinction between animals vaccinated with conventional vaccine strains
 XX from that of animals immunised with a vaccine based in this NDV mutant.
 XX The NDV vaccine is useful in chickens, as well as in other poultry, e.g.
 XX turkey, pigeons, quails, pheasants, guinea fowl or partridges.
 XX All currently used whole virus based live and inactivated
 XX ND vaccines have a major drawback, in that vaccinated animals cannot be
 XX distinguished from infected animals with standard serological tests
 XX (e.g. haemagglutination inhibition or virus neutralisation). The present
 XX NDV immunogenic mutant, being a marker vaccine, enables serological
 XX differentiation of vaccinated animals from infected animals. The use of
 XX the present NDV mutant as an embryo vaccine is also proven as effective
 XX and economical due to the early age of resistance to a specific
 XX disease. The present sequence represents a PCR primer used to
 XX delete DNA corresponding to amino acids 442-489 of the nucleoprotein.
 XX Sequence 35 BP; 12 A; 10 C; 11 G; 2 T; 0 other;
 XX
 XX Query Match 0.9%; Score 20.6; DB 24; Length 35;
 XX Best Local Similarity 74.3%; Pred. No. 1.2e+05;
 XX Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 XX
 XX QY 1313 GGCMAAAGATCCCAATGTTGACMAAACACAGC 1347
 XX 1 GCCAACCCAGAGCGCGGTGATGACMAAACCCAGC 35
 XX
 XX RESULT 45
 XX ABR6582/c
 XX ID ABR6582 standard; DNA; 35 BP.
 XX ABR6582;
 XX 24-SEP-2002 (first entry)
 XX Newcastle disease virus nucleoprotein mutagenic PCR primer P3B.
 XX Nucleoprotein; NP; immunodominant epitope; newcastle disease; poultry;
 XX virucide; ND; vaccine; ovo administration; ss; PCR; primer.
 XX Newcastle disease virus.
 XX WO200236617-A2.
 XX 10-MAY-2002.
 XX

```

PF 30-OCT-2001; 2001WO-EP12573.
XX
PR 02-NOV-2000; 2000EP-0203814.
XX
PA (ALKU ) AKZO NOBEL NV.
XX
PI Mebatson T, Koolen MJM;
XX
PS WPI: 2002-527441/56.
XX
PT New Newcastle disease virus (NDV) mutant, useful as a vaccine for
PT protecting poultry (e.g. chicken) against Newcastle disease or as a
PT marker vaccine to distinguish vaccinated animals from those infected
PT with naturally occurring NDV
XX
PS Example 1; Page 15; 51pp; English.
XX
CC The invention relates to a Newcastle disease virus (NDV) mutant, which
CC lacks an immunogenic epitope on a NDV protein as a result of a mutation
CC in a gene encoding the protein, where the NDV mutant lacks an epitope
CC located within a regions (amino acids 447-455 and 443-460) of the
CC nucleoprotein (NP). Also included are a vaccine against Newcastle disease
CC (NDV) in poultry comprising the DNA mutant in a live or inactivated form,
CC and a pharmaceutical carrier or diluent and determining NDV infection in
CC poultry by examining a sample of the animal for the presence or absence
CC of antibodies reactive with the immunodominant epitope located within the
CC region of the NP. The NDV mutant is useful as a vaccine for protecting a
CC poultry against ND in poultry. Particularly for in ovo administration a
CC vaccine against ND in poultry.
CC The vaccine is also useful in a ND control program to distinguish
CC vaccinated animals from animals infected with naturally occurring NDV
CC The NDV mutant is also useful as a marker vaccine to allow serological
CC distinction between animals vaccinated with conventional vaccine strains
CC from that of animals immunised with a vaccine based in this NDV mutant.
CC The NDV vaccine is useful in chickens, as well as in other poultry, e.g.
CC turkey, pigeons, quails, pheasants, guinea fowl or partridges.
CC All currently used whole virus based live and inactivated
CC ND vaccines have a major drawback, in that vaccinated animals cannot be
CC distinguished from infected animals with standard serological tests
CC (e.g. haemagglutination inhibition or virus neutralisation). The present
CC NDV immunogenic mutant, being a marker vaccine, enables serological
CC differentiation of vaccinated animals from infected animals. The use of
CC the present NDV mutant as an embryo vaccine is also proven as effective
CC and economical due to the early age of resistance to a specific
CC disease. The present sequence represents a PCR primer used to
CC delete DNA corresponding to amino acids 442-489 of the nucleoprotein.
XX
SQ Sequence 35 BP; 2 A; 11 C; 10 G; 12 T; 0 other;
XX
Query Match 0.9%; Score 20.6; DB 24; Length 35;
Best Local Similarity 74.3%; Pred. No. 1.2e+05;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
OY 1313 GGCACAAAAGAAATCCCAATGTTGACAAACACAGC 1347
DB 35 GGCACACGAGAGCGCGGTGATGACAAACCCAGC 1
XX
RESULT 46
ID AA267746 standard; DNA; 47 BP.
XX
AC AA267746;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human map-related biallelic marker SEQ ID NO:2093.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW diagnosis; single nucleotide polymorphism; SNP; ds.
XX

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OS Homo sapiens.
XX
XX Key Location/Qualifiers
FT variation replace(24,6)
FT /tag= a
FT /standard_name= "single nucleotide polymorphism"
XX
PN M09954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB00822.
XX
PR 21-APR-1998; 98US-0082614.
XX
PR 23-NOV-1998; 98US-0109732.
XX
PA (GEST ) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI: 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome
XX
PS Claim 1; Page 677; 2745pp; English.
XX
CC AA265654 to AA269578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AA269579 to AA277440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the
CC invention have a variety of uses: they can be used for high density
CC mapping of the human genome, and in complex association studies and
CC haplotyping studies which are useful in determining the genetic basis
CC for disease states. Compositions and methods of the invention can also
CC be useful for the identification of the targets for the development of
CC pharmaceutical agents and diagnostic methods, as well as the
CC characterisation of the differential efficacious responses to and side
CC effects from pharmaceutical agents acting on a disease as well as other
CC treatment.
CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
CC and 3367, are not actually given a sequence in the Sequence Listing
CC from the present invention.
XX
SQ Sequence 47 BP; 13 A; 18 C; 11 G; 5 T; 0 other;
XX
Query Match 0.9%; Score 20.6; DB 21; Length 47;
Best Local Similarity 74.3%; Pred. No. 1.4e+05;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
OY 1872 GCCACCTCACCAAGAGACCTTGGAGAGCAGAGGAC 1906
DB 1 GTCACCTCACCCAGGAGAGGACGCAAGAGCTAGGAC 35
XX
RESULT 47
ID AAL30421/c
XX
AC AAL30421 standard; DNA; 50 BP.
XX
AC AAL30421;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #3629.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinase; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX

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XX OS Homo sapiens.
XX PN WO200147944-A2.
XX PD 05-JUL-2001.
XX PF 28-DEC-2000; 2000MO-US35498.
XX PR 28-DEC-1999; 99US-0173419.
XX PR 27-DEC-2000; 2000US-0173419.
XX PA (CURA-) CURAGEN CORP.
XX PI Shinkets RA, Leach M;
XX DR WPI: 2001-465210/50.
XX PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX PT oncogenes and histones, useful for diagnosing and treating, e.g.
XX PT cancer, autoimmune diseases and infections -
XX PS Claim 1: Page 2428; 4143pp; English.
XX CC The present invention relates to oligonucleotides encoding polymorphic
XX CC variants of proteins related to amylases, amyloid proteins, angiotensin,
XX CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
XX CC histones, kinases, colony stimulating factors, complement related
XX CC proteins, cytochromes, kinases, cytokines, interferons, interleukins,
XX CC G-protein coupled receptors and thioesterases. The present sequence is
XX CC one such oligonucleotide. The oligonucleotides and the peptides encoded
XX CC by them may be used in the prevention, diagnosis and treatment of
XX CC diseases associated with inappropriate expression of the proteins listed
XX CC above. Disorders that may be prevented, diagnosed and/or treated include
XX CC multifactorial diseases with a genetic component, such as autoimmune
XX CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
XX CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
XX CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
XX CC leukaemia), diseases of the nervous system and an infection of pathogenic
XX CC organisms.
XX
SQ Sequence 50 BP; 15 A; 13 C; 7 G; 15 T; 0 other;
Query Match 0.9%; Score 20.6; DB 22; Length 50;
Best Local Similarity 74.3%; Pred. No. 1.4e+05;
Matches 26; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 2201 AAGATGCTGTTACTTTTGCAATCTTGATTAATGA 2235
DB 37 AGGAGGTGTGATTGTTTGCATTCGACAAAGA 3
RESULT 48
AAI79057/C
ID AAI79057 standard; DNA: 50 BP.
XX AC AAI79057;
XX DT 09-NOV-2001 (first entry)
XX DE Human silent SNP containing nucleic acid SEQ.5998.
XX OS Homo sapiens.
XX PN WO200140521-A2.
XX PD 07-JUN-2001.
XX PF 30-NOV-2000; 2000MO-US32758.

XX PR 30-NOV-1999; 99US-0168138.
XX PR 29-NOV-2000; 2000US-0726173.
XX PA (CURA-) CURAGEN CORP.
XX PI Shinkets RA, Leach M;
XX DR WPI: 2001-356160/37.
XX PT Polymorphic nucleic acid sequences, useful in genetic testing and
XX PT therapy -
XX PS Claim 1: Page 2345; 2653pp; English.
XX CC AAI73060 to AAI79867 represent isolated human polymorphic polynucleotide
XX CC sequences (1), which contain single nucleotide polymorphisms (SNPs).
XX CC AAM53114 to AAM53329 represent peptides related to human polymorphic
XX CC polynucleotide sequences. The sequences can be used in gene and protein
XX CC therapy, and in vaccine production. (1) and the polypeptides encoded by
XX CC them may be used in the prevention, diagnosis and treatment of diseases
XX CC associated with inappropriate expression of polymorphic polypeptides.
XX CC For example, (1) may be used to treat disorders by rectifying mutations
XX CC or deletions in a patient's genome that affect the activity of
XX CC polypeptides by expressing inactive proteins or to supplement the
XX CC patients own production of polypeptide. Additionally, (1) and its
XX CC complementary sequences may also be used as DNA probes in diagnostic
XX CC assays to detect and quantitate the presence of similar nucleic acids
XX CC in samples, and therefore which patients may be in need of restorative
XX CC therapy. The polypeptides encoded by (1) may be used as antigens in the
XX CC production of antibodies specific for polymorphic polypeptides. The
XX CC antibodies may also be used to down regulate expression and activity.
XX CC The antibodies may also be used as diagnostic agents for detecting the
XX CC presence of polymorphic polypeptides in samples.
XX
SQ Sequence 50 BP; 26 A; 4 C; 16 G; 4 T; 0 other;
Query Match 0.9%; Score 20.6; DB 22; Length 50;
Best Local Similarity 67.4%; Pred. No. 1.4e+05;
Matches 29; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 1093 CTTTCGTGCTGCTCTTTGTTCTCTGAATTTTCAGACACTTT 1135
DB 43 CTTTCCTGCTCTGCTCTCTTTCTTTCTTTTGATAGAACT 1
RESULT 49
AAV68378/C
ID AAV68378 standard; DNA: 50 BP.
XX AC AAV68378;
XX DT 10-MAR-1999 (first entry)
XX DE Clone #4 fragment identified by CAG repeat analysis method.4.
XX OS Homo sapiens.
XX PN WO9849345-A1.
XX PD 05-NOV-1998.
XX PF 29-APR-1998; 98WO-US08616.
XX PR 29-APR-1997; 97US-0045078.
XX PA (UYBO-) UNIV BOSTON.
XX PI Smith CL;

